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<p>(54) Title: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE BREAST</p>		
<p>(57) Abstract</p> <p>A set of contiguous and partially overlapping cDNA sequences and polypeptides encoded thereby, designated as BS200 and transcribed from breast tissue, is described. These sequences are useful for the detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition of an individual to diseases and conditions of the breast, such as breast cancer. Also provided are antibodies which specifically bind to BS200-encoded polypeptide or protein, and agonists or inhibitors which prevent action of the tissue-specific BS200 polypeptide, which molecules are useful for the therapeutic treatment of breast diseases, tumors or metastases.</p>		

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REAGENTS AND METHODS USEFUL FOR DETECTING  
DISEASES OF THE BREAST

Background of the Invention

This invention relates generally to detecting diseases of the breast. Furthermore, the invention also relates to reagents and methods for detecting diseases of the breast. More particularly, the present invention relates to reagents such as polynucleotide sequences and the polypeptide sequences encoded thereby, as well as methods which utilize these sequences. The polynucleotide and polypeptide sequences are useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer.

Breast cancer is the most common form of cancer occurring in females in the U.S. The incidence of breast cancers in the United States is projected to be 180,300 cases diagnosed and 43,900 breast cancer-related deaths to occur during 1998 (American Cancer Society statistics). Worldwide, the incidence of breast cancer increased from 700,000 in 1985 to about 900,000 in 1990. G.N. Hortobagyi et al., CA Cancer J Clin 45: 199-226 (1995).

Procedures used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer, are of critical importance to the outcome of the patient. For example, patients diagnosed with early breast cancer have greater than a 90% five-year relative survival rate as compared to a survival rate of about 20% for patients diagnosed with distantly metastasized breast cancers. (American Cancer Society statistics). Currently, the best initial indicators of early breast cancer are physical examination of the breast and mammography. J.R. Harris et al. In: Cancer: Principles and Practice of Oncology, Fourth Edition, pp. 1264-1332, Philadelphia, PA: J/B. Lippincott Co. (1993). Mammography may detect a breast tumor before it can be detected by physical examination, but it has

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limitations. For example, mammography's predictive value depends on the observer's skill and the quality of the mammogram. In addition, 80 to 93% of suspicious mammograms are false positives, and 10 to 15% of women with breast cancer have false negative mammograms. C.J. Wright et al., Lancet 346: 29-32 (1995). New diagnostic methods which are more sensitive and specific for detecting early breast cancer are clearly needed.

Breast cancer patients are closely monitored following initial therapy and during adjuvant therapy to determine response to therapy, and to detect persistent or recurrent disease, or early distant metastasis. Current diagnostic procedures for monitoring breast cancer include mammography, bone scan, chest radiographs, liver function tests and tests for serum markers. The serum tumor markers most commonly used for monitoring patients are carcinoembryonic antigen (CEA) and CA 15-3. Limitations of CEA include absence of elevated serum levels in about 40% of women with metastatic disease. In addition, CEA elevation during adjuvant therapy may not be related to recurrence but to other factors that are not clinically important. CA 15-3 can also be negative in a significant number of patients with progressive disease and, therefore, fail to predict metastasis. Both CEA and CA 15-3 can be elevated in nonmalignant, benign conditions giving rise to false positive results. Therefore, it would be clinically beneficial to find a breast associated marker which is more sensitive and specific in detecting cancer recurrence. J. R. Harris et al., supra. M. K. Schwartz, In: Cancer: Principles and Practice of Oncology, Vol. 1, Fourth Edition, pp. 531 - 542, Philadelphia, PA: J/B. Lippincott Co. 1993.

Another important step in managing breast cancer is to determine the stage of the patient's disease because stage determination has potential prognostic value and provides criteria for designing optimal therapy. Currently, pathological staging of breast cancer is preferable over clinical staging because the former gives a more accurate prognosis. J. R. Harris et al., supra. On the other hand, clinical staging would be preferred were it at least as accurate as pathological staging because it does not depend on an invasive procedure to obtain tissue for pathological evaluation. Staging of breast cancer could be improved by detecting new markers in serum or urine which could differentiate between different stages of invasion. Such markers could be mRNA or protein markers expressed by cells originating from the primary tumor in the breast but residing in blood, bone marrow or

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lymph nodes and could serve as sensitive indicators for metastasis to these distal organs. For example, specific protein antigens and mRNA, associated with breast epithelial cells, have been detected by immunohistochemical techniques and RT-PCR, respectively, in bone marrow, lymph nodes and blood of breast cancer patients suggesting metastasis. K. Pantel et al., Onkologie 18: 394-401 (1995).

Such diagnostic procedures also could include immunological assays based upon the appearance of various disease markers in test samples such as blood, plasma, serum or urine obtained by minimally invasive procedures which are detectable by immunological methods. These diagnostic procedures would provide information to aid the physician in managing the patient with disease of the breast, at low cost to the patient. Markers such as prostate specific antigen (PSA) and human chorionic gonadotropin (hCG) exist and are used clinically for screening patients for prostate cancer and testicular cancer, respectively. For example, PSA normally is secreted by the prostate at high levels into the seminal fluid, but is present in very low levels in the blood of men with normal prostates. Elevated levels of PSA protein in serum are used in the early detection of prostate cancer or disease in asymptomatic men. See, for example, G.E. Hanks et al., In: *Cancer: Principles and Practice of Oncology*, Vol. 1, Fourth Edition, pp. 1073-1113, Philadelphia, PA: J.B. Lippincott Co. 1993. M. K. Schwartz et al., In: *Cancer: Principles and Practice of Oncology*, Vol. 1, Fourth Edition, pp. 531-542, Philadelphia, PA: J.B. Lippincott Co. 1993. Likewise, the management of breast diseases could be improved by the use of new markers normally expressed in the breast but found in elevated amounts in an inappropriate body compartment as a result of the disease of the breast.

Further, new markers which could predict the biologic behavior of early breast cancers would also be of significant value. Early breast cancers that threaten or will threaten the life of the patient are more clinically important than those that do not or will not be a threat. G.E. Hanks, *supra*. Such markers are needed to predict which patients with histologically negative lymph nodes will experience recurrence of cancer and also to predict which cases of ductal carcinoma in situ will develop into invasive breast carcinoma. More accurate prognostic markers would allow the clinician to accurately identify early cancers localized to the breast which will progress and metastasize if not treated aggressively. Additionally, the absence of a marker for an aggressive cancer in the patient could spare the

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patient expensive and non-beneficial treatment. J. R. Harris et al., supra. E. R. Frykberg et al., Cancer 74: 350-361 (1994).

It therefore would be advantageous to provide specific methods and reagents useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining predisposition to diseases or conditions of the breast. Such methods would include assaying a test sample for products of a gene which are overexpressed in diseases and conditions associated with the breast, including cancer. Such methods may also include assaying a test sample for products of a gene which have been altered by the disease or condition associated with the breast, including cancer. Such methods may further include assaying a test sample for products of a gene whose distribution among the various tissues and compartments of the body have been altered by a breast-associated disease or condition, including cancer. Such methods would comprise making cDNA from mRNA in the test sample, amplifying, when necessary, portions of the cDNA corresponding to the gene or a fragment thereof, and detecting the cDNA product as an indication of the presence of the disease or condition including cancer or detecting translation products of the mRNAs comprising gene sequences as an indication of the presence of the disease. Useful reagents include polynucleotide(s), or fragment(s) thereof which may be used in diagnostic methods such as reverse transcriptase-polymerase chain reaction (RT-PCR), PCR, or hybridization assays of mRNA extracted from biopsied tissue, blood or other test samples; or proteins which are the translation products of such mRNAs; or antibodies directed against these proteins. Such assays would include methods for assaying a sample for product(s) of the gene and detecting the product(s) as an indication of disease of the breast. Drug treatment or gene therapy for diseases and conditions of the breast including cancer can be based on these identified gene sequences or their expressed proteins, and efficacy of any particular therapy can be monitored. Furthermore, it would be advantageous to have available alternative, non-surgical diagnostic methods capable of detecting early stage breast disease, such as cancer.

#### Summary of the Invention

The present invention provides a method of detecting a target BS200 polynucleotide in a test sample which comprises contacting the test sample with

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at least one BS200-specific polynucleotide and detecting the presence of the target BS200 polynucleotide in the test sample. The BS200-specific polynucleotide has at least 50% identity with a polynucleotide selected from the group consisting of SEQUENCE ID NO 1, SEQUENCE ID NO 2, SEQUENCE ID NO 3, SEQUENCE ID NO 4, SEQUENCE ID NO 5, SEQUENCE ID NO 6, SEQUENCE ID NO 7, SEQUENCE ID NO 8, SEQUENCE ID NO 9, SEQUENCE ID NO 10, SEQUENCE ID NO 11, SEQUENCE ID NO 12, SEQUENCE ID NO 13, SEQUENCE ID NO 14, SEQUENCE ID NO 15, SEQUENCE ID NO 16 ("SEQUENCE ID NOS 1-16"), and fragments or complements thereof. Also, the BS200-specific polynucleotide may be attached to a solid phase prior to performing the method.

The present invention also provides a method for detecting BS200 mRNA in a test sample, which comprises performing reverse transcription (RT) with at least one primer in order to produce cDNA, amplifying the cDNA so obtained using BS200 oligonucleotides as sense and antisense primers to obtain BS200 amplicon, and detecting the presence of the BS200 amplicon as an indication of the presence of BS200 mRNA in the test sample, wherein the BS200 oligonucleotides have at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof. Amplification can be performed by the polymerase chain reaction. Also, the test sample can be reacted with a solid phase prior to performing the method, prior to amplification or prior to detection. This reaction can be a direct or an indirect reaction. Further, the detection step can comprise utilizing a detectable label capable of generating a measurable signal. The detectable label can be attached to a solid phase.

The present invention further provides a method of detecting a target BS200 polynucleotide in a test sample suspected of containing target BS200 polynucleotides, which comprises (a) contacting the test sample with at least one BS200 oligonucleotide as a sense primer and at least one BS200 oligonucleotide as an anti-sense primer, and amplifying same to obtain a first stage reaction product; (b) contacting the first stage reaction product with at least one other BS200 oligonucleotide to obtain a second stage reaction product, with the proviso that the other BS200 oligonucleotide is located 3' to the BS200 oligonucleotides utilized in step (a) and is complementary to the first stage reaction product; and (c) detecting the second stage reaction product as an indication of the presence of a target BS200 polynucleotide in the test sample.

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The BS200 oligonucleotides selected as reagents in the method have at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof. Amplification may be performed by the polymerase chain reaction. The test sample can be reacted either directly or indirectly with a solid phase prior to performing the method, or prior to amplification, or prior to detection. The detection step also comprises utilizing a detectable label capable of generating a measurable signal; further, the detectable label can be attached to a solid phase. Test kits useful for detecting target BS200 polynucleotides in a test sample are also provided which comprise a container containing at least one BS200-specific polynucleotide selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof. These test kits further comprise containers with tools useful for collecting test samples (such as, for example, blood, urine, saliva and stool). Such tools include lancets and absorbent paper or cloth for collecting and stabilizing blood; swabs for collecting and stabilizing saliva; and cups for collecting and stabilizing urine or stool samples. Collection materials, such as papers, cloths, swabs, cups, and the like, may optionally be treated to avoid denaturation or irreversible adsorption of the sample. The collection materials also may be treated with or contain preservatives, stabilizers or antimicrobial agents to help maintain the integrity of the specimens.

The present invention also provides a purified polynucleotide or fragment thereof derived from a BS200 gene. The purified polynucleotide is capable of selectively hybridizing to the nucleic acid of the BS200 gene, or a complement thereof. The polynucleotide has at least 50% identity with a polynucleotide selected from the group consisting of: (a) SEQUENCE ID NOS 1-7, SEQUENCE ID NO 9, SEQUENCE ID NOS 11-12, SEQUENCE ID NOS 14-16, and complements thereof; and (b) fragments of SEQUENCE ID NOS 1-14. Further, the purified polynucleotide can be produced by recombinant and/or synthetic techniques. The purified recombinant polynucleotide can be contained within a recombinant vector. The invention further comprises a host cell transfected with the recombinant vector.

The present invention further provides a recombinant expression system comprising a nucleic acid sequence that includes an open reading frame derived from BS200. The nucleic acid sequence has at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof. The nucleic acid sequence is operably linked



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to a control sequence compatible with a desired host. Also provided is a cell transfected with this recombinant expression system.

The present invention also provides a polypeptide encoded by BS200. The polypeptide can be produced by recombinant technology, provided in purified form, or produced by synthetic techniques. The polypeptide comprises an amino acid sequence which has at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

Also provided is an antibody which specifically binds to at least one BS200 epitope. The antibody can be a polyclonal or monoclonal antibody. The epitope is derived from an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. Assay kits for determining the presence of BS200 antigen or anti-BS200 antibody in a test sample are also included. In one embodiment, the assay kits comprise a container containing at least one BS200 polypeptide having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. Further, the test kit can comprise a container with tools useful for collecting test samples (such as blood, urine, saliva, and stool). Such tools include lancets and absorbent paper or cloth for collecting and stabilizing blood; swabs for collecting and stabilizing saliva; and cups for collecting and stabilizing urine or stool samples. Collection materials such as papers, cloths, swabs, cups, and the like, may optionally be treated to avoid denaturation or irreversible adsorption of the sample. These collection materials also may be treated with or contain preservatives, stabilizers or antimicrobial agents to help maintain the integrity of the specimens. Also, the polypeptide can be attached to a solid phase.

In another embodiment of the invention, antibodies or fragments thereof against the BS200 antigen can be used to detect or image localization of the antigen in a patient for the purpose of detecting or diagnosing a disease or condition. Such antibodies can be polyclonal or monoclonal, or made by molecular biology techniques, and can be labeled with a variety of detectable labels, including but not limited to radioisotopes and paramagnetic metals. Furthermore, antibodies or fragments thereof, whether monoclonal, polyclonal,

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or made by molecular biology techniques, can be used as therapeutic agents for the treatment of diseases characterized by expression of the BS200 antigen. In the case of therapeutic applications, the antibody may be used without derivitization, or it may be derivitized with a cytotoxic agent such as a radioisotope, enzyme, toxin, drug, prodrug, or the like.

Another assay kit for determining the presence of BS200 antigen or anti-BS200 antibody in a test sample comprises a container containing an antibody which specifically binds to a BS200 antigen, wherein the BS200 antigen comprises at least one BS200-encoded epitope. The BS200 antigen has at least about 60% sequence similarity to a sequence of a BS200-encoded antigen selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. These test kits can further comprise containers with tools useful for collecting test samples (such as blood, urine, saliva, and stool). Such tools include lancets and absorbent paper or cloth for collecting and stabilizing blood; swabs for collecting and stabilizing saliva; cups for collecting and stabilizing urine or stool samples. Collection materials, such as papers, cloths, swabs, cups and the like, may optionally be treated to avoid denaturation or irreversible adsorption of the sample. These collection materials also may be treated with, or contain, preservatives, stabilizers or antimicrobial agents to help maintain the integrity of the specimens. The antibody can be attached to a solid phase.

A method for producing a polypeptide which contains at least one epitope of BS200 is provided, which method comprises incubating host cells transfected with an expression vector. This vector comprises a polynucleotide sequence encoding a polypeptide, wherein the polypeptide comprises an amino acid sequence having at least 50% identity with a BS200 amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

A method for detecting BS200 antigen in a test sample suspected of containing BS200 antigen also is provided. The method comprises contacting the test sample with an antibody or fragment thereof which specifically binds to at least one epitope of BS200 antigen, for a time and under conditions sufficient for the formation of antibody/antigen complexes; and detecting the presence of such complexes containing the antibody as an indication of the presence of

BS200 antigen in the test sample. The antibody can be attached to a solid phase and may be either a monoclonal or polyclonal antibody. Furthermore, the antibody specifically binds to at least one BS200 antigen selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

Another method is provided which detects antibodies which specifically bind to BS200 antigen in a test sample suspected of containing these antibodies. The method comprises contacting the test sample with a polypeptide which contains at least one BS200 epitope, wherein the BS200 epitope comprises an amino acid sequence having at least 50% identity with an amino acid sequence encoded by a BS200 polynucleotide, or a fragment thereof. Contacting is carried out for a time and under conditions sufficient to allow antigen/antibody complexes to form. The method further entails detecting complexes which contain the polypeptide. The polypeptide can be attached to a solid phase. Further, the polypeptide can be a recombinant protein or a synthetic peptide having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

The present invention provides a cell transfected with a BS200 nucleic acid sequence that encodes at least one epitope of a BS200 antigen, or fragment thereof. The nucleic acid sequence is selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof.

A method for producing antibodies to BS200 antigen also is provided, which method comprises administering to an individual an isolated immunogenic polypeptide or fragment thereof, wherein the isolated immunogenic polypeptide comprises at least one BS200 epitope. The immunogenic polypeptide is administered in an amount sufficient to produce an immune response. The isolated, immunogenic polypeptide comprises an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

Another method for producing antibodies which specifically bind to BS200 antigen is disclosed, which method comprises administering to an individual a plasmid comprising a nucleic acid sequence which encodes at least one BS200 epitope derived from an amino acid sequence selected from the

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group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. The plasmid is administered in an amount such that the plasmid is taken up by cells in the individual and expressed at levels sufficient to produce an immune response.

Also provided is a composition of matter that comprises a BS200 polynucleotide of at least about 10-12 nucleotides and having at least 50% identity with a polynucleotide selected from the group consisting of: (a) SEQUENCE ID NOS 1-7, SEQUENCE ID NO 9, SEQUENCE ID NOS 11-12, SEQUENCE ID NOS 14-16, and complements thereof; and (b) fragments of SEQUENCE ID NOS 1- 14. The BS200 polynucleotide encodes an amino acid sequence having at least one BS200 epitope. Another composition of matter provided by the present invention comprises a polypeptide with at least one BS200 epitope of about 8-10 amino acids. The polypeptide comprises an amino acid sequence having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. Also provided is a gene, or a fragment thereof, coding for a BS200 polypeptide which has at least 50% identity to SEQUENCE ID NO 31; and a gene, or a fragment thereof, comprising DNA having at least 50% identity with SEQUENCE ID NO 15 or SEQUENCE ID NO 16.

#### Brief Description of the Drawings

Figures 1A-1E show the nucleotide alignment of clones 2767006 (SEQUENCE ID NO 1), 3021177 (SEQUENCE ID NO 2), 3213801 (SEQUENCE ID NO 3), 2224165 (SEQUENCE ID NO 4), 1316156 (SEQUENCE ID NO 5), 1549512 (SEQUENCE ID NO 6), 1919065 (SEQUENCE ID NO 7), g898160 (SEQUENCE ID NO 8), 2116945 (SEQUENCE ID NO 9), g1985883 (SEQUENCE ID NO 10), 1925574 (SEQUENCE ID NO 11), 3724828 (SEQUENCE ID NO 12), g1444044 (SEQUENCE ID NO 13), 1808382 (SEQUENCE ID NO 14), and the full-length sequence of clone 3021177 (designated as clone 3021177IH (SEQUENCE ID NO 15)), and the consensus sequence (SEQUENCE ID NO 16) derived therefrom.

Figure 2 shows the contig map depicting the formation of the consensus nucleotide sequence (SEQUENCE ID NO 16) from the nucleotide alignment of

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overlapping clones 2767006 (SEQUENCE ID NO 1), 3021177 (SEQUENCE ID NO 2), 3213801 (SEQUENCE ID NO 3), 2224165 (SEQUENCE ID NO 4), 1316156 (SEQUENCE ID NO 5), 1549512 (SEQUENCE ID NO 6), 1919065 (SEQUENCE ID NO 7), g898160 (SEQUENCE ID NO 8), 2116945 (SEQUENCE ID NO 9), g1985883 (SEQUENCE ID NO 10), 1925574 (SEQUENCE ID NO 11), 3724828 (SEQUENCE ID NO 12), g1444044 (SEQUENCE ID NO 13), 1808382 (SEQUENCE ID NO 14), and 3021177IH (SEQUENCE ID NO 15).

Figure 3A is a scan of an ethidium bromide-stained electrophoresis gel of BS200 RNA specific RT-PCR amplification products from normal breast and breast cancer tissue RNAs. Figure 3B is a scan of an ethidium bromide-stained electrophoresis gel of BS200 RNA-specific RT-PCR amplification products from RNAs of normal or cancer tissues of the lung and colon.

#### Detailed Description of the Invention

The present invention provides a gene, or a fragment thereof, which codes for a BS200 polypeptide having at least about 50% identity to SEQUENCE ID NO 31. The present invention further encompasses a BS200 gene, or a fragment thereof, comprising DNA which has at least about 50% identity with SEQUENCE ID NO 15 or SEQUENCE ID NO 16.

The present invention also provides methods for assaying a test sample for products of a breast tissue gene designated as BS200, which comprises making cDNA from mRNA in the test sample, and detecting the cDNA as an indication of the presence of breast tissue gene BS200. The method may include an amplification step, wherein one or more portions of the mRNA from BS200 corresponding to the gene or fragments thereof, is amplified. Methods also are provided for assaying for the translation products of BS200. Test samples which may be assayed by the methods provided herein include tissues, cells, body fluids and secretions. The present invention also provides reagents such as oligonucleotide primers and polypeptides which are useful in performing these methods.

Portions of the nucleic acid sequences disclosed herein are useful as primers for the reverse transcription of RNA or for the amplification of cDNA; or as probes to determine the presence of certain mRNA sequences in test samples. Also disclosed are nucleic acid sequences which permit the production of encoded polypeptide sequences which are useful as standards or reagents in

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diagnostic immunoassays, as targets for pharmaceutical screening assays and/or as components or as target sites for various therapies. Monoclonal and polyclonal antibodies directed against at least one epitope contained within these polypeptide sequences are useful as delivery agents for therapeutic agents as well as for diagnostic tests and for screening for diseases or conditions associated with BS200, especially breast cancer. Isolation of sequences of other portions of the gene of interest can be accomplished utilizing probes or PCR primers derived from these nucleic acid sequences. This allows additional probes of the mRNA or cDNA of interest to be established, as well as corresponding encoded polypeptide sequences. These additional molecules are useful in detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to diseases and conditions of the breast, such as breast cancer, characterized by BS200, as disclosed herein.

Techniques for determining amino acid sequence "similarity" are well-known in the art. In general, "similarity" means the exact amino acid to amino acid comparison of two or more polypeptides at the appropriate place, where amino acids are identical or possess similar chemical and/or physical properties such as charge or hydrophobicity. A so-termed "percent similarity" then can be determined between the compared polypeptide sequences. Techniques for determining nucleic acid and amino acid sequence identity also are well known in the art and include determining the nucleotide sequence of the mRNA for that gene (usually via a cDNA intermediate) and determining the amino acid sequence encoded thereby, and comparing this to a second amino acid sequence. In general, "identity" refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of two polynucleotides or polypeptide sequences, respectively. Two or more polynucleotide sequences can be compared by determining their "percent identity." Two or more amino acid sequences likewise can be compared by determining their "percent identity." The percent identity of two sequences, whether nucleic acid or peptide sequences, is the number of exact matches between two aligned sequences divided by the length of the shorter sequences and multiplied by 100. An approximate alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981). This algorithm can be extended to use with peptide sequences using the scoring matrix developed by Dayhoff, Atlas of Protein Sequences and Structure, M.O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation,

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Washington, D.C., USA, and normalized by Gribskov, Nucl. Acids Res. 14(6):6745-6763 (1986). An implementation of this algorithm for nucleic acid and peptide sequences is provided by the Genetics Computer Group (Madison, WI) in their BestFit utility application. The default parameters for this method are described in the Wisconsin Sequence Analysis Package Program Manual, Version 8 (1995) (available from Genetics Computer Group, Madison, WI). Other equally suitable programs for calculating the percent identity or similarity between sequences are generally known in the art.

The compositions and methods described herein will enable the identification of certain markers as indicative of a breast tissue disease or condition; the information obtained therefrom will aid in the detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining diseases or conditions associated with BS200, especially breast cancer. Test methods include, for example, probe assays which utilize the sequence(s) provided herein and which also may utilize nucleic acid amplification methods such as the polymerase chain reaction (PCR), the ligase chain reaction (LCR), and hybridization. In addition, the nucleotide sequences provided herein contain open reading frames from which an immunogenic epitope may be found. This epitope is believed to be unique to the disease state or condition associated with BS200. It also is thought that the polynucleotides or polypeptides and protein encoded by the BS200 gene are useful as a marker. This marker is either elevated in disease such as breast cancer, altered in disease such as breast cancer, or present as a normal protein but appearing in an inappropriate body compartment. The uniqueness of the epitope may be determined by (i) its immunological reactivity and specificity with antibodies directed against proteins and polypeptides encoded by the BS200 gene, and (ii) its nonreactivity with any other tissue markers. Methods for determining immunological reactivity are well-known and include, but are not limited to, for example, radioimmunoassay (RIA), enzyme-linked immunoabsorbent assay (ELISA), hemagglutination (HA), fluorescence polarization immunoassay (FPIA), chemiluminescent immunoassay (CLIA) and others. Several examples of suitable methods are described herein.

Unless otherwise stated, the following terms shall have the following meanings:

A polynucleotide "derived from" or "specific for" a designated sequence refers to a polynucleotide sequence which comprises a contiguous sequence of

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approximately at least about 6 nucleotides, preferably at least about 8 nucleotides, more preferably at least about 10-12 nucleotides, and even more preferably at least about 15-20 nucleotides corresponding, i.e., identical or complementary to, a region of the designated nucleotide sequence. The sequence may be complementary or identical to a sequence which is unique to a particular polynucleotide sequence as determined by techniques known in the art. Comparisons to sequences in databanks, for example, can be used as a method to determine the uniqueness of a designated sequence. Regions from which sequences may be derived, include but are not limited to, regions encoding specific epitopes, as well as non-translated and/or non-transcribed regions.

The derived polynucleotide will not necessarily be derived physically from the nucleotide sequence of interest under study, but may be generated in any manner, including, but not limited to, chemical synthesis, replication, reverse transcription or transcription, which is based on the information provided by the sequence of bases in the region(s) from which the polynucleotide is derived. As such, it may represent either a sense or an antisense orientation of the original polynucleotide. In addition, combinations of regions corresponding to that of the designated sequence may be modified in ways known in the art to be consistent with the intended use.

A "fragment" of a specified polynucleotide refers to a polynucleotide sequence which comprises a contiguous sequence of approximately at least about 6 nucleotides, preferably at least about 8 nucleotides, more preferably at least about 10-12 nucleotides, and even more preferably at least about 15-20 nucleotides corresponding, i.e., identical or complementary to, a region of the specified nucleotide sequence.

The term "primer" denotes a specific oligonucleotide sequence which is complementary to a target nucleotide sequence and used to hybridize to the target nucleotide sequence. A primer serves as an initiation point for nucleotide polymerization catalyzed by either DNA polymerase, RNA polymerase or reverse transcriptase.

The term "probe" denotes a defined nucleic acid segment (or nucleotide analog segment, e.g., PNA as defined hereinbelow) which can be used to identify a specific polynucleotide present in samples bearing the complementary sequence.

"Encoded by" refers to a nucleic acid sequence which codes for a polypeptide sequence, wherein the polypeptide sequence or a portion thereof



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contains an amino acid sequence of at least 3 to 5 amino acids, more preferably at least 8 to 10 amino acids, and even more preferably at least 15 to 20 amino acids from a polypeptide encoded by the nucleic acid sequence. Also encompassed are polypeptide sequences which are immunologically identifiable with a polypeptide encoded by the sequence. Thus, a "polypeptide," "protein," or "amino acid" sequence has at least about 50% identity, preferably about 60% identity, more preferably about 75-85% identity, and most preferably about 90-95% or more identity to a BS200 amino acid sequence. Further, the BS200 "polypeptide," "protein," or "amino acid" sequence may have at least about 60% similarity, preferably at least about 75% similarity, more preferably about 85% similarity, and most preferably about 95% or more similarity to a polypeptide or amino acid sequence of BS200. This amino acid sequence can be selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

A "recombinant polypeptide," "recombinant protein," or "a polypeptide produced by recombinant techniques," which terms may be used interchangeably herein, describes a polypeptide which by virtue of its origin or manipulation is not associated with all or a portion of the polypeptide with which it is associated in nature and/or is linked to a polypeptide other than that to which it is linked in nature. A recombinant or encoded polypeptide or protein is not necessarily translated from a designated nucleic acid sequence. It also may be generated in any manner, including chemical synthesis or expression of a recombinant expression system.

The term "synthetic peptide" as used herein means a polymeric form of amino acids of any length, which may be chemically synthesized by methods well-known to the routineer. These synthetic peptides are useful in various applications.

The term "polynucleotide" as used herein means a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, the term includes double- and single-stranded DNA, as well as double- and single-stranded RNA. It also includes modifications, such as methylation or capping and unmodified forms of the polynucleotide. The terms "polynucleotide," "oligomer," "oligonucleotide," and "oligo" are used interchangeably herein.

"A sequence corresponding to a cDNA" means that the sequence contains a polynucleotide sequence that is identical or complementary to a sequence in the designated DNA. The degree (or "percent") of identity or complementarity to the cDNA will be approximately 50% or greater, preferably at least about 70% or greater, and more preferably at least about 90% or greater. The sequence that corresponds to the identified cDNA will be at least about 50 nucleotides in length, preferably at least about 60 nucleotides in length, and more preferably at least about 70 nucleotides in length. The correspondence between the gene or gene fragment of interest and the cDNA can be determined by methods known in the art and include, for example, a direct comparison of the sequenced material with the cDNAs described, or hybridization and digestion with single strand nucleases, followed by size determination of the digested fragments.

"Purified polynucleotide" refers to a polynucleotide of interest or fragment thereof which is essentially free, e.g., contains less than about 50%, preferably less than about 70%, and more preferably less than about 90%, of the protein with which the polynucleotide is naturally associated. Techniques for purifying polynucleotides of interest are well-known in the art and include, for example, disruption of the cell containing the polynucleotide with a chaotropic agent and separation of the polynucleotide(s) and proteins by ion-exchange chromatography, affinity chromatography and sedimentation according to density.

"Purified polypeptide" or "purified protein" means a polypeptide of interest or fragment thereof which is essentially free of, e.g., contains less than about 50%, preferably less than about 70%, and more preferably less than about 90%, cellular components with which the polypeptide of interest is naturally associated. Methods for purifying polypeptides of interest are known in the art.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or DNA or polypeptide, which is separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotide could be part of a vector and/or such polynucleotide or polypeptide could be part of a composition, and still be isolated in that the vector or composition is not part of its natural environment.

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"Polypeptide" and "protein" are used interchangeably herein and indicate at least one molecular chain of amino acids linked through covalent and/or non-covalent bonds. The terms do not refer to a specific length of the product. Thus peptides, oligopeptides and proteins are included within the definition of polypeptide. The terms include post-translational modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like. In addition, protein fragments, analogs, mutated or variant proteins, fusion proteins and the like are included within the meaning of polypeptide.

A "fragment" of a specified polypeptide refers to an amino acid sequence which comprises at least about 3-5 amino acids, more preferably at least about 8-10 amino acids, and even more preferably at least about 15-20 amino acids derived from the specified polypeptide.

"Recombinant host cells," "host cells," "cells," "cell lines," "cell cultures," and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refer to cells which can be, or have been, used as recipients for recombinant vector or other transferred DNA, and include the original progeny of the original cell which has been transfected.

As used herein "replicon" means any genetic element, such as a plasmid, a chromosome or a virus, that behaves as an autonomous unit of polynucleotide replication within a cell.

A "vector" is a replicon in which another polynucleotide segment is attached, such as to bring about the replication and/or expression of the attached segment.

The term "control sequence" refers to a polynucleotide sequence which is necessary to effect the expression of a coding sequence to which it is ligated. The nature of such control sequences differs depending upon the host organism. In prokaryotes, such control sequences generally include a promoter, a ribosomal binding site and terminators; in eukaryotes, such control sequences generally include promoters, terminators and, in some instances, enhancers. The term "control sequence" thus is intended to include at a minimum all components whose presence is necessary for expression, and also may include additional components whose presence is advantageous, for example, leader sequences.

"Operably linked" refers to a situation wherein the components described are in a relationship permitting them to function in their intended manner. Thus, for example, a control sequence "operably linked" to a coding sequence is

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ligated in such a manner that expression of the coding sequence is achieved under conditions compatible with the control sequence.

The term "open reading frame" or "ORF" refers to a region of a polynucleotide sequence which encodes a polypeptide. This region may represent a portion of a coding sequence or a total coding sequence.

A "coding sequence" is a polynucleotide sequence which is transcribed into mRNA and translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5' -terminus and a translation stop codon at the 3' -terminus. A coding sequence can include, but is not limited to, mRNA, cDNA and recombinant polynucleotide sequences.

The term "immunologically identifiable with/as" refers to the presence of epitope(s) and polypeptide(s) which also are present in and are unique to the designated polypeptide(s). Immunological identity may be determined by antibody binding and/or competition in binding. These techniques are known to the routineer and also are described herein. The uniqueness of an epitope also can be determined by computer searches of known data banks, such as GenBank, for the polynucleotide sequence which encodes the epitope and by amino acid sequence comparisons with other known proteins.

As used herein, "epitope" means an antigenic determinant of a polypeptide or protein. Conceivably, an epitope can comprise three amino acids in a spatial conformation which is unique to the epitope. Generally, an epitope consists of at least five such amino acids and more usually, it consists of at least eight to ten amino acids. Methods of examining spatial conformation are known in the art and include, for example, x-ray crystallography and two-dimensional nuclear magnetic resonance.

A "conformational epitope" is an epitope that is comprised of a specific juxtaposition of amino acids in an immunologically recognizable structure, such amino acids being present on the same polypeptide in a contiguous or non-contiguous order or present on different polypeptides.

A polypeptide is "immunologically reactive" with an antibody when it binds to an antibody due to antibody recognition of a specific epitope contained within the polypeptide. Immunological reactivity may be determined by antibody binding, more particularly, by the kinetics of antibody binding, and/or by competition in binding using as competitor(s) a known polypeptide(s) containing an epitope against which the antibody is directed. The methods for

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determining whether a polypeptide is immunologically reactive with an antibody are known in the art.

As used herein, the term "immunogenic polypeptide containing an epitope of interest" means naturally occurring polypeptides of interest or fragments thereof, as well as polypeptides prepared by other means, for example, by chemical synthesis or the expression of the polypeptide in a recombinant organism.

The term "transfection" refers to the introduction of an exogenous polynucleotide into a prokaryotic or eucaryotic host cell, irrespective of the method used for the introduction. The term "transfection" refers to both stable and transient introduction of the polynucleotide, and encompasses direct uptake of polynucleotides, transformation, transduction, and f-mating. Once introduced into the host cell, the exogenous polynucleotide may be maintained as a non-integrated replicon, for example, a plasmid, or alternatively, may be integrated into the host genome.

"Treatment" refers to prophylaxis and/or therapy.

The term "individual" as used herein refers to vertebrates, particularly members of the mammalian species and includes, but is not limited to, domestic animals, sports animals, primates and humans; more particularly, the term refers to humans.

The term "sense strand" or "plus strand" (or "+") as used herein denotes a nucleic acid that contains the sequence that encodes the polypeptide. The term "antisense strand" or "minus strand" (or "-") denotes a nucleic acid that contains a sequence that is complementary to that of the "plus" strand.

The term "test sample" refers to a component of an individual's body which is the source of the analyte (such as antibodies of interest or antigens of interest). These components are well known in the art. A test sample is typically anything suspected of containing a target sequence. Test samples can be prepared using methodologies well known in the art such as by obtaining a specimen from an individual and, if necessary, disrupting any cells contained thereby to release target nucleic acids. These test samples include biological samples which can be tested by the methods of the present invention described herein and include human and animal body fluids such as whole blood, serum, plasma, cerebrospinal fluid, sputum, bronchial washing, bronchial aspirates, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitourinary tracts, tears, saliva, milk, white blood cells, myelomas and the

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like; biological fluids such as cell culture supernatants; tissue specimens which may be fixed; and cell specimens which may be fixed.

"Purified product" refers to a preparation of the product which has been isolated from the cellular constituents with which the product is normally associated and from other types of cells which may be present in the sample of interest.

"PNA" denotes a "peptide nucleic acid analog" which may be utilized in a procedure such as an assay described herein to determine the presence of a target. "MA" denotes a "morpholino analog" which may be utilized in a procedure such as an assay described herein to determine the presence of a target. See, for example, U.S. Patent No. 5,378,841. PNAs are neutrally charged moieties which can be directed against RNA targets or DNA. PNA probes used in assays in place of, for example, the DNA probes of the present invention, offer advantages not achievable when DNA probes are used. These advantages include manufacturability, large scale labeling, reproducibility, stability, insensitivity to changes in ionic strength and resistance to enzymatic degradation which is present in methods utilizing DNA or RNA. These PNAs can be labeled with ("attached to") such signal generating compounds as fluorescein, radionucleotides, chemiluminescent compounds and the like. PNAs or other nucleic acid analogs such as MAs thus can be used in assay methods in place of DNA or RNA. Although assays are described herein utilizing DNA probes, it is within the scope of the routineer that PNAs or MAs can be substituted for RNA or DNA with appropriate changes if and as needed in assay reagents.

"Analyte," as used herein, is the substance to be detected which may be present in the test sample. The analyte can be any substance for which there exists a naturally occurring specific binding member (such as an antibody), or for which a specific binding member can be prepared. Thus, an analyte is a substance that can bind to one or more specific binding members in an assay. "Analyte" also includes any antigenic substances, haptens, antibodies and combinations thereof. As a member of a specific binding pair, the analyte can be detected by means of naturally occurring specific binding partners (pairs) such as the use of intrinsic factor protein as a member of a specific binding pair for the determination of Vitamin B12, the use of folate-binding protein to determine folic acid, or the use of a lectin as a member of a specific binding pair for the determination of a carbohydrate. The analyte can include a protein, a

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polypeptide, an amino acid, a nucleotide target and the like. The analyte can be soluble in a body fluid such as blood, blood plasma or serum, urine or the like. The analyte can be in a tissue, either on a cell surface or within a cell. The analyte can be on or in a cell dispersed in a body fluid such as blood, urine, breast aspirate, or obtained as a biopsy sample.

The terms "diseases of the breast," "breast disease," and "condition of the breast" are used interchangeably herein to refer to any disease or condition of the breast including, but not limited to, atypical hyperplasia, fibroadenoma, cystic breast disease, and cancer.

"Breast cancer," as used herein, refers to any malignant disease of the breast including, but not limited to, ductal carcinoma in situ, lobular carcinoma in situ, infiltrating ductal carcinoma, medullary carcinoma, tubular carcinoma, mucinous carcinoma, infiltrating lobular carcinoma, infiltrating comedocarcinoma and inflammatory carcinoma.

An "Expressed Sequence Tag" or "EST" refers to the partial sequence of a cDNA insert which has been made by reverse transcription of mRNA extracted from a tissue followed by insertion into a vector.

A "transcript image" refers to a table or list giving the quantitative distribution of ESTs in a library and represents the genes active in the tissue from which the library was made.

The present invention provides assays which utilize specific binding members. A "specific binding member," as used herein, is a member of a specific binding pair. That is, two different molecules where one of the molecules, through chemical or physical means, specifically binds to the second molecule. Therefore, in addition to antigen and antibody specific binding pairs of common immunoassays, other specific binding pairs can include biotin and avidin, carbohydrates and lectins, complementary nucleotide sequences, effector and receptor molecules, cofactors and enzymes, enzyme inhibitors, and enzymes and the like. Furthermore, specific binding pairs can include members that are analogs of the original specific binding members, for example, an analyte-analog. Immunoreactive specific binding members include antigens, antigen fragments, antibodies and antibody fragments, both monoclonal and polyclonal and complexes thereof, including those formed by recombinant DNA molecules.

The term "hapten," as used herein, refers to a partial antigen or non-protein binding member which is capable of binding to an antibody, but which is not capable of eliciting antibody formation unless coupled to a carrier protein.

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A "capture reagent," as used herein, refers to an unlabeled specific binding member which is specific either for the analyte as in a sandwich assay, for the indicator reagent or analyte as in a competitive assay, or for an ancillary specific binding member, which itself is specific for the analyte, as in an indirect assay. The capture reagent can be directly or indirectly bound to a solid phase material before the performance of the assay or during the performance of the assay, thereby enabling the separation of immobilized complexes from the test sample.

The "indicator reagent" comprises a "signal-generating compound" ("label") which is capable of generating and generates a measurable signal detectable by external means, conjugated ("attached") to a specific binding member. In addition to being an antibody member of a specific binding pair, the indicator reagent also can be a member of any specific binding pair, including either hapten-anti-hapten systems such as biotin or anti-biotin, avidin or biotin, a carbohydrate or a lectin, a complementary nucleotide sequence, an effector or a receptor molecule, an enzyme cofactor and an enzyme, an enzyme inhibitor or an enzyme and the like. An immunoreactive specific binding member can be an antibody, an antigen, or an antibody/antigen complex that is capable of binding either to the polypeptide of interest as in a sandwich assay, to the capture reagent as in a competitive assay, or to the ancillary specific binding member as in an indirect assay. When describing probes and probe assays, the term "reporter molecule" may be used. A reporter molecule comprises a signal generating compound as described hereinabove conjugated to a specific binding member of a specific binding pair, such as carbazole or adamantane.

The various "signal-generating compounds" (labels) contemplated include chromagens, catalysts such as enzymes, luminescent compounds such as fluorescein and rhodamine, chemiluminescent compounds such as dioxetanes, acridiniums, phenanthridiniums and luminol, radioactive elements and direct visual labels. Examples of enzymes include alkaline phosphatase, horseradish peroxidase, beta-galactosidase and the like. The selection of a particular label is not critical, but it must be capable of producing a signal either by itself or in conjunction with one or more additional substances.

"Solid phases" ("solid supports") are known to those in the art and include the walls of wells of a reaction tray, test tubes, polystyrene beads, magnetic or non-magnetic beads, nitrocellulose strips, membranes, microparticles such as latex particles, sheep (or other animal) red blood cells and



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Duracytes<sup>®</sup> (red blood cells "fixed" by pyruvic aldehyde and formaldehyde, available from Abbott Laboratories, Abbott Park, IL) and others. The "solid phase" is not critical and can be selected by one skilled in the art. Thus, latex particles, microparticles, magnetic or non-magnetic beads, membranes, plastic tubes, walls of microtiter wells, glass or silicon chips, sheep (or other suitable animal's) red blood cells and Duracytes<sup>®</sup> are all suitable examples. Suitable methods for immobilizing peptides on solid phases include ionic, hydrophobic, covalent interactions and the like. A "solid phase," as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid phase can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid phase and which has the ability to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid phase material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal's) red blood cells, Duracytes<sup>®</sup> and other configurations known to those of ordinary skill in the art.

It is contemplated and within the scope of the present invention that the solid phase also can comprise any suitable porous material with sufficient porosity to allow access by detection antibodies and a suitable surface affinity to bind antigens. Microporous structures generally are preferred, but materials with a gel structure in the hydrated state may be used as well. Such useful solid supports include, but are not limited to, nitrocellulose and nylon. It is contemplated that such porous solid supports described herein preferably are in the form of sheets of thickness from about 0.01 to 0.5 mm, preferably about 0.1 mm. The pore size may vary within wide limits and preferably is from about 0.025 to 15 microns, especially from about 0.15 to 15 microns. The surface of such supports may be activated by chemical processes which cause covalent linkage of the antigen or antibody to the support. The irreversible binding of the

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antigen or antibody is obtained, however, in general, by adsorption on the porous material by poorly understood hydrophobic forces. Other suitable solid supports are known in the art.

#### Reagents.

The present invention provides reagents such as polynucleotide sequences derived from a breast tissue of interest and designated as BS200, polypeptides encoded thereby and antibodies specific for these polypeptides. The present invention also provides reagents such as oligonucleotide fragments derived from the disclosed polynucleotides and nucleic acid sequences complementary to these polynucleotides. The polynucleotides, polypeptides, or antibodies of the present invention may be used to provide information leading to the detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating of, or determining the predisposition to, diseases and conditions of the breast, such as breast cancer. The sequences disclosed herein represent unique polynucleotides which can be used in assays or for producing a specific profile of gene transcription activity. Such assays are disclosed in European Patent Number 0373203B1 and International Publication No. WO 95/11995.

Selected BS200-derived polynucleotides can be used in the methods described herein for the detection of normal or altered gene expression. Such methods may employ BS200 polynucleotides or oligonucleotides, fragments or derivatives thereof, or nucleic acid sequences complementary thereto.

The polynucleotides disclosed herein, their complementary sequences, or fragments of either, can be used in assays to detect, amplify or quantify genes, nucleic acids, cDNAs or mRNAs relating to breast tissue disease and conditions associated therewith. They also can be used to identify an entire or partial coding region of a BS200 polypeptide. They further can be provided in individual containers in the form of a kit for assays, or provided as individual compositions. If provided in a kit for assays, other suitable reagents such as buffers, conjugates and the like may be included.

The polynucleotide may be in the form of RNA or DNA. Polynucleotides in the form of DNA, cDNA, genomic DNA, nucleic acid analogs and synthetic DNA are within the scope of the present invention. The DNA may be double-stranded or single-stranded, and if single stranded, may be the coding (sense) strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide may be identical to the coding sequence provided herein or may be a different coding sequence which coding sequence,

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as a result of the redundancy or degeneracy of the genetic code, encodes the same polypeptide as the DNA provided herein.

This polynucleotide may include only the coding sequence for the polypeptide, or the coding sequence for the polypeptide and an additional coding sequence such as a leader or secretory sequence or a proprotein sequence, or the coding sequence for the polypeptide (and optionally an additional coding sequence) and non-coding sequence, such as a non-coding sequence 5' and/or 3' of the coding sequence for the polypeptide.

In addition, the invention includes variant polynucleotides containing modifications such as polynucleotide deletions, substitutions or additions; and any polypeptide modification resulting from the variant polynucleotide sequence. A polynucleotide of the present invention also may have a coding sequence which is a naturally occurring allelic variant of the coding sequence provided herein.

In addition, the coding sequence for the polypeptide may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the polypeptide. The polynucleotides may also encode for a proprotein which is the protein plus additional 5' amino acid residues. A protein having a prosequence is a proprotein and may, in some cases, be an inactive form of the protein. Once the prosequence is cleaved, an active protein remains. Thus, the polynucleotide of the present invention may encode for a protein, or for a protein having a prosequence, or for a protein having both a prosequence (leader sequence) and a prosequence.

The polynucleotides of the present invention may also have the coding sequence fused in frame to a marker sequence which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexahistidine tag supplied by a pQE-9 vector to provide for purification of the polypeptide fused to the marker in the case of a bacterial host, or, for example, the marker sequence may be a hemagglutinin (HA) tag when a mammalian host, e.g. a COS-7 cell line, is used. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein. See, for example, I. Wilson et al., Cell 37:767 (1984).

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It is contemplated that polynucleotides will be considered to hybridize to the sequences provided herein if there is at least 50%, preferably at least 70%, and more preferably at least 90% identity between the polynucleotide and the sequence.

The present invention also provides an antibody produced by using a purified BS200 polypeptide of which at least a portion of the polypeptide is encoded by a BS200 polynucleotide selected from the polynucleotides provided herein. These antibodies may be used in the methods provided herein for the detection of BS200 antigen in test samples. The presence of BS200 antigen in the test samples is indicative of the presence of a breast disease or condition. The antibody also may be used for therapeutic purposes, for example, in neutralizing the activity of BS200 polypeptide in conditions associated with altered or abnormal expression.

The present invention further relates to a BS200 polypeptide which has the deduced amino acid sequence as provided herein, as well as fragments, analogs and derivatives of such polypeptide. The polypeptide of the present invention may be a recombinant polypeptide, a natural purified polypeptide or a synthetic polypeptide. The fragment, derivative or analog of the BS200 polypeptide may be one in which one or more of the amino acid residues is substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code; or it may be one in which one or more of the amino acid residues includes a substituent group; or it may be one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol); or it may be one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are within the scope of the present invention. The polypeptides and polynucleotides of the present invention are provided preferably in an isolated form and preferably purified.

Thus, a polypeptide of the present invention may have an amino acid sequence that is identical to that of the naturally occurring polypeptide or that is different by minor variations due to one or more amino acid substitutions. The variation may be a "conservative change" typically in the range of about 1 to 5 amino acids, wherein the substituted amino acid has similar structural or

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chemical properties, e.g., replacement of leucine with isoleucine or threonine with serine. In contrast, variations may include nonconservative changes, e.g., replacement of a glycine with a tryptophan. Similar minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which and how many amino acid residues may be substituted, inserted or deleted without changing biological or immunological activity may be found using computer programs well known in the art, for example, DNASTAR software (DNASTAR Inc., Madison WI).

Probes constructed according to the polynucleotide sequences of the present invention can be used in various assay methods to provide various types of analysis. For example, such probes can be used in fluorescent in situ hybridization (FISH) technology to perform chromosomal analysis, and used to identify cancer-specific structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR-generated and/or allele specific oligonucleotides probes, allele specific amplification or by direct sequencing. Probes also can be labeled with radioisotopes, directly- or indirectly- detectable haptens, or fluorescent molecules, and utilized for in situ hybridization studies to evaluate the mRNA expression of the gene comprising the polynucleotide in tissue specimens or cells.

This invention also provides teachings as to the production of the polynucleotides and polypeptides provided herein.

#### Probe Assays

The sequences provided herein may be used to produce probes which can be used in assays for the detection of nucleic acids in test samples. The probes may be designed from conserved nucleotide regions of the polynucleotides of interest or from non-conserved nucleotide regions of the polynucleotide of interest. The design of such probes for optimization in assays is within the skill of the routineer. Generally, nucleic acid probes are developed from non-conserved or unique regions when maximum specificity is desired, and nucleic acid probes are developed from conserved regions when assaying for nucleotide regions that are closely related to, for example, different members of a multi-gene family or in related species like mouse and man.

The polymerase chain reaction (PCR) is a technique for amplifying a desired nucleic acid sequence (target) contained in a nucleic acid or mixture thereof. In PCR, a pair of primers are employed in excess to hybridize to the

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complementary strands of the target nucleic acid. The primers are each extended by a polymerase using the target nucleic acid as a template. The extension products become target sequences themselves, following dissociation from the original target strand. New primers then are hybridized and extended by a polymerase, and the cycle is repeated to geometrically increase the number of target sequence molecules. PCR is disclosed in U.S. Patents 4,683,195 and 4,683,202.

The Ligase Chain Reaction (LCR) is an alternate method for nucleic acid amplification. In LCR, probe pairs are used which include two primary (first and second) and two secondary (third and fourth) probes, all of which are employed in molar excess to target. The first probe hybridizes to a first segment of the target strand, and the second probe hybridizes to a second segment of the target strand, the first and second segments being contiguous so that the primary probes abut one another in 5' phosphate-3' hydroxyl relationship, and so that a ligase can covalently fuse or ligate the two probes into a fused product. In addition, a third (secondary) probe can hybridize to a portion of the first probe and a fourth (secondary) probe can hybridize to a portion of the second probe in a similar abutting fashion. Of course, if the target is initially double stranded, the secondary probes also will hybridize to the target complement in the first instance. Once the ligated strand of primary probes is separated from the target strand, it will hybridize with the third and fourth probes which can be ligated to form a complementary, secondary ligated product. It is important to realize that the ligated products are functionally equivalent to either the target or its complement. By repeated cycles of hybridization and ligation, amplification of the target sequence is achieved. This technique is described more completely in EP-A- 320 308 to K. Backman published June 16, 1989 and EP-A-439 182 to K. Backman et al., published July 31, 1991.

For amplification of mRNAs, it is within the scope of the present invention to reverse transcribe mRNA into cDNA followed by polymerase chain reaction (RT-PCR); or, to use a single enzyme for both steps as described in U.S. Patent No. 5,322,770; or reverse transcribe mRNA into cDNA followed by asymmetric gap ligase chain reaction (RT-AGLCR) as described by R.L. Marshall et al., PCR Methods and Applications 4: 80-84 (1994).

Other known amplification methods which can be utilized herein include but are not limited to the so-called "NASBA" or "3SR" technique described by J.C. Guatelli et al., PNAS USA 87:1874-1878 (1990) and also described by J.

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Compton, Nature 350 (No. 6313):91-92 (1991); Q-beta amplification as described in published European Patent Application (EPA) No. 4544610; strand displacement amplification (as described in G.T. Walker et al., Clin. Chem. 42:9-13 [1996]) and European Patent Application No. 684315; and target mediated amplification, as described in International Publication No. WO 93/22461.

Detection of BS200 may be accomplished using any suitable detection method, including those detection methods which are currently well known in the art, as well as detection strategies which may evolve later. See, for example, Caskey et al., U.S. Patent No. 5,582,989, Gelfand et al., U.S. Patent No. 5,210,015. Examples of such detection methods include target amplification methods as well as signal amplification technologies. An example of presently known detection methods would include the nucleic acid amplification technologies referred to as PCR, LCR, NASBA, SDA, RCR and TMA. See, for example, Caskey et al., U.S. Patent No. 5,582,989, Gelfand et al., U.S. Patent No. 5,210,015. Detection may also be accomplished using signal amplification such as that disclosed in Snitman et al., U.S. Patent No. 5,273,882. While the amplification of target or signal is preferred at present, it is contemplated and within the scope of the present invention that ultrasensitive detection methods which do not require amplification can be utilized herein.

Detection, both amplified and non-amplified, may be (combined) carried out using a variety of heterogeneous and homogeneous detection formats. Examples of heterogeneous detection formats are disclosed in Snitman et al., U.S. Patent No. 5,273,882, Albarella et al., in EP-841 14441.9, Urdea et al., U.S. Patent No. 5,124,246, Ullman et al. U.S. Patent No. 5,185,243 and Kourilsky et al., U.S. Patent No. 4,581,333. Examples of homogeneous detection formats are disclosed in, Caskey et al., U.S. Patent No. 5,582,989, Gelfand et al., U.S. Patent No. 5,210,015. Also contemplated and within the scope of the present invention is the use of multiple probes in the hybridization assay, which use improves sensitivity and amplification of the BS200 signal. See, for example, Caskey et al., U.S. Patent No. 5,582,989, Gelfand et al., U.S. Patent No. 5,210,015.

In one embodiment, the present invention generally comprises the steps of contacting a test sample suspected of containing a target polynucleotide sequence with amplification reaction reagents comprising an amplification primer, and a detection probe that can hybridize with an internal region of the amplicon sequences. Probes and primers employed according to the method

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provided herein are labeled with capture and detection labels, wherein probes are labeled with one type of label and primers are labeled with another type of label. Additionally, the primers and probes are selected such that the probe sequence has a lower melt temperature than the primer sequences. The amplification reagents, detection reagents and test sample are placed under amplification conditions whereby, in the presence of target sequence, copies of the target sequence (an amplicon) are produced. In the usual case, the amplicon is double stranded because primers are provided to amplify a target sequence and its complementary strand. The double stranded amplicon then is thermally denatured to produce single stranded amplicon members. Upon formation of the single stranded amplicon members, the mixture is cooled to allow the formation of complexes between the probes and single stranded amplicon members.

As the single stranded amplicon sequences and probe sequences are cooled, the probe sequences preferentially bind the single stranded amplicon members. This finding is counterintuitive given that the probe sequences generally are selected to be shorter than the primer sequences and therefore have a lower melt temperature than the primers. Accordingly, the melt temperature of the amplicon produced by the primers should also have a higher melt temperature than the probes. Thus, as the mixture cools, the re-formation of the double stranded amplicon would be expected. As previously stated, however, this is not the case. The probes are found to preferentially bind the single stranded amplicon members. Moreover, this preference of probe/single stranded amplicon binding exists even when the primer sequences are added in excess of the probes.

After the probe/single stranded amplicon member hybrids are formed, they are detected. Standard heterogeneous assay formats are suitable for detecting the hybrids using the detection labels and capture labels present on the primers and probes. The hybrids can be bound to a solid phase reagent by virtue of the capture label and detected by virtue of the detection label. In cases where the detection label is directly detectable, the presence of the hybrids on the solid phase can be detected by causing the label to produce a detectable signal, if necessary, and detecting the signal. In cases where the label is not directly detectable, the captured hybrids can be contacted with a conjugate, which generally comprises a binding member attached to a directly detectable label. The conjugate becomes bound to the complexes and the conjugate's presence on the complexes can be detected with the directly detectable label. Thus, the



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presence of the hybrids on the solid phase reagent can be determined. Those skilled in the art will recognize that wash steps may be employed to wash away unhybridized amplicon or probe as well as unbound conjugate.

Although the target sequence is described as single stranded, it also is contemplated to include the case where the target sequence is actually double stranded but is merely separated from its complement prior to hybridization with the amplification primer sequences. In the case where PCR is employed in this method, the ends of the target sequences are usually known. In cases where LCR or a modification thereof is employed in the preferred method, the entire target sequence is usually known. Typically, the target sequence is a nucleic acid sequence such as, for example, RNA or DNA.

The method provided herein can be used in well-known amplification reactions that include thermal cycle reaction mixtures, particularly in PCR and gap LCR (GLCR). Amplification reactions typically employ primers to repeatedly generate copies of a target nucleic acid sequence, which target sequence is usually a small region of a much larger nucleic acid sequence. Primers are themselves nucleic acid sequences that are complementary to regions of a target sequence. Under amplification conditions, these primers hybridize or bind to the complementary regions of the target sequence. Copies of the target sequence typically are generated by the process of primer extension and/or ligation which utilizes enzymes with polymerase or ligase activity, separately or in combination, to add nucleotides to the hybridized primers and/or ligate adjacent probe pairs. The nucleotides that are added to the primers or probes, as monomers or preformed oligomers, are also complementary to the target sequence. Once the primers or probes have been sufficiently extended and/or ligated, they are separated from the target sequence, for example, by heating the reaction mixture to a "melt temperature" which is one in which complementary nucleic acid strands dissociate. Thus, a sequence complementary to the target sequence is formed.

A new amplification cycle then can take place to further amplify the number of target sequences by separating any double stranded sequences, allowing primers or probes to hybridize to their respective targets, extending and/or ligating the hybridized primers or probes and re-separating. The complementary sequences that are generated by amplification cycles can serve as templates for primer extension or filling the gap of two-probes to further amplify the number of target sequences. Typically, a reaction mixture is cycled between

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20 and 100 times, more typically, a reaction mixture is cycled between 25 and 50 times. The numbers of cycles can be determined by the routineer. In this manner, multiple copies of the target sequence and its complementary sequence are produced. Thus, primers initiate amplification of the target sequence when it is present under amplification conditions.

Generally, two primers which are complementary to a portion of a target strand and its complement are employed in PCR. For LCR, four probes, two of which are complementary to a target sequence and two of which are similarly complementary to the target's complement, are generally employed. In addition to the primer sets and enzymes previously mentioned, a nucleic acid amplification reaction mixture may also comprise other reagents which are well known and include but are not limited to: enzyme cofactors such as manganese; magnesium; salts; nicotinamide adenine dinucleotide (NAD); and deoxynucleotide triphosphates (dNTPs) such as, for example, deoxyadenine triphosphate, deoxyguanine triphosphate, deoxycytosine triphosphate and deoxythymine triphosphate.

While the amplification primers initiate amplification of the target sequence, the detection (or hybridization) probe is not involved in amplification. Detection probes are generally nucleic acid sequences or uncharged nucleic acid analogs such as, for example, peptide nucleic acids which are disclosed in International Publication No. WO 92/20702; morpholino analogs which are described in U.S. Patents Nos 5,185,444, 5,034,506 and 5,142,047; and the like. Depending upon the type of label carried by the probe, the probe is employed to capture or detect the amplicon generated by the amplification reaction. The probe is not involved in amplification of the target sequence and therefore may have to be rendered "non-extendible" in that additional dNTPs cannot be added to the probe. In and of themselves, analogs usually are non-extendible and nucleic acid probes can be rendered non-extendible by modifying the 3' end of the probe such that the hydroxyl group is no longer capable of participating in elongation. For example, the 3' end of the probe can be functionalized with the capture or detection label to thereby consume or otherwise block the hydroxyl group. Alternatively, the 3' hydroxyl group simply can be cleaved, replaced or modified. U.S. Patent Application Serial No. 07/049,061 filed April 19, describes modifications which can be used to render a probe non-extendible.

The ratio of primers to probes is not important. Thus, either the probes or primers can be added to the reaction mixture in excess whereby the

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concentration of one would be greater than the concentration of the other. Alternatively, primers and probes can be employed in equivalent concentrations. Preferably, however, the primers are added to the reaction mixture in excess of the probes. Thus, primer to probe ratios of, for example, 5:1 and 20:1, are preferred.

While the length of the primers and probes can vary, the probe sequences are selected such that they have a lower melt temperature than the primer sequences. Hence, the primer sequences are generally longer than the probe sequences. Typically, the primer sequences are in the range of between 20 and 50 nucleotides long, more typically in the range of between 20 and 30 nucleotides long. The typical probe is in the range of between 10 and 25 nucleotides long.

Various methods for synthesizing primers and probes are well known in the art. Similarly, methods for attaching labels to primers or probes are also well known in the art. For example, it is a matter of routine to synthesize desired nucleic acid primers or probes using conventional nucleotide phosphoramidite chemistry and instruments available from Applied Biosystems, Inc., (Foster City, CA), DuPont (Wilmington, DE), or Milligen (Bedford MA). Many methods have been described for labeling oligonucleotides such as the primers or probes of the present invention. Enzo Biochemical (New York, NY) and Clontech (Palo Alto, CA) both have described and commercialized probe labeling techniques. For example, a primary amine can be attached to a 3' oligo terminus using 3'-Amine-ON CPG™ (Clontech, Palo Alto, CA). Similarly, a primary amine can be attached to a 5' oligo terminus using Aminomodifier II® (Clontech). The amines can be reacted to various haptens using conventional activation and linking chemistries. In addition, copending applications U.S. Serial Nos. 625,566, filed December 11, 1990 and 630,908, filed December 20, 1990, teach methods for labeling probes at their 5' and 3' termini, respectively. International Publication Nos WO 92/10505, published 25 June 1992, and WO 92/11388, published 9 July 1992, teach methods for labeling probes at their 5' and 3' ends, respectively. According to one known method for labeling an oligonucleotide, a label-phosphoramidite reagent is prepared and used to add the label to the oligonucleotide during its synthesis. See, for example, N.T. Thuong et al., *Tet. Letters* 29(46):5905-5908 (1988); or J.S. Cohen et al., published U.S. Patent Application 07/246,688 (NTIS ORDER No. PAT-APPL-7-246,688) (1989). Preferably, probes are labeled at their 3' and 5' ends.

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A capture label is attached to the primers or probes and can be a specific binding member which forms a binding pair with the solid phase reagent's specific binding member. It will be understood that the primer or probe itself may serve as the capture label. For example, in the case where a solid phase reagent's binding member is a nucleic acid sequence, it may be selected such that it binds a complementary portion of the primer or probe to thereby immobilize the primer or probe to the solid phase. In cases where the probe itself serves as the binding member, those skilled in the art will recognize that the probe will contain a sequence or "tail" that is not complementary to the single stranded amplicon members. In the case where the primer itself serves as the capture label, at least a portion of the primer will be free to hybridize with a nucleic acid on a solid phase because the probe is selected such that it is not fully complementary to the primer sequence.

Generally, probe/single stranded amplicon member complexes can be detected using techniques commonly employed to perform heterogeneous immunoassays. Preferably, in this embodiment, detection is performed according to the protocols used by the commercially available Abbott LCx<sup>®</sup> instrumentation (Abbott Laboratories, Abbott Park, IL).

The primers and probes disclosed herein are useful in typical PCR assays, wherein the test sample is contacted with a pair of primers, amplification is performed, the hybridization probe is added, and detection is performed.

Another method provided by the present invention comprises contacting a test sample with a plurality of polynucleotides, wherein at least one polynucleotide is a BS200 molecule as described herein, hybridizing the test sample with the plurality of polynucleotides and detecting hybridization complexes. Hybridization complexes are identified and quantitated to compile a profile which is indicative of breast tissue disease, such as breast cancer. Expressed RNA sequences may further be detected by reverse transcription and amplification of the DNA product by procedures well-known in the art, including polymerase chain reaction (PCR).

#### Drug Screening and Gene Therapy.

The present invention also encompasses the use of gene therapy methods for the introduction of anti-sense BS200 derived molecules, such as polynucleotides or oligonucleotides of the present invention, into patients with conditions associated with abnormal expression of polynucleotides related to a breast tissue disease or condition especially breast cancer. These molecules,

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including antisense RNA and DNA fragments and ribozymes, are designed to inhibit the translation of BS200 mRNA, and may be used therapeutically in the treatment of conditions associated with altered or abnormal expression of BS200 polynucleotide.

Alternatively, the oligonucleotides described above can be delivered to cells by procedures known in the art such that the anti-sense RNA or DNA may be expressed in vivo to inhibit production of a BS200 polypeptide in the manner described above. Antisense constructs to a BS200 polynucleotide, therefore, reverse the action of BS200 transcripts and may be used for treating breast tissue disease conditions, such as breast cancer. These antisense constructs may also be used to treat tumor metastases.

The present invention also provides a method of screening a plurality of compounds for specific binding to BS200 polypeptide(s), or any fragment thereof, to identify at least one compound which specifically binds the BS200 polypeptide. Such a method comprises the steps of providing at least one compound; combining the BS200 polypeptide with each compound under suitable conditions for a time sufficient to allow binding; and detecting the BS200 polypeptide binding to each compound.

The polypeptide or peptide fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of screening utilizes eukaryotic or prokaryotic host cells which are stably transfected with recombinant nucleic acids which can express the polypeptide or peptide fragment. A drug, compound, or any other agent may be screened against such transfected cells in competitive binding assays. For example, the formation of complexes between a polypeptide and the agent being tested can be measured in either viable or fixed cells.

The present invention thus provides methods of screening for drugs, compounds, or any other agent which can be used to treat diseases associated with BS200. These methods comprise contacting the agent with a polypeptide or fragment thereof and assaying for either the presence of a complex between the agent and the polypeptide, or for the presence of a complex between the polypeptide and the cell. In competitive binding assays, the polypeptide typically is labeled. After suitable incubation, free (or uncomplexed) polypeptide or fragment thereof is separated from that present in bound form, and the amount of free or uncomplexed label is used as a measure of the ability

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of the particular agent to bind to the polypeptide or to interfere with the polypeptide/cell complex.

The present invention also encompasses the use of competitive screening assays in which neutralizing antibodies capable of binding polypeptide specifically compete with a test agent for binding to the polypeptide or fragment thereof. In this manner, the antibodies can be used to detect the presence of any polypeptide in the test sample which shares one or more antigenic determinants with a BS200 polypeptide as provided herein.

Another technique for screening provides high throughput screening for compounds having suitable binding affinity to at least one polypeptide of BS200 disclosed herein. Briefly, large numbers of different small peptide test compounds are synthesized on a solid phase, such as plastic pins or some other surface. The peptide test compounds are reacted with polypeptide and washed. Polypeptide thus bound to the solid phase is detected by methods well-known in the art. Purified polypeptide can also be coated directly onto plates for use in the screening techniques described herein. In addition, non-neutralizing antibodies can be used to capture the polypeptide and immobilize it on the solid support. See, for example, EP 84/03564, published on September 13, 1984.

The goal of rational drug design is to produce structural analogs of biologically active polypeptides of interest or of the small molecules including agonists, antagonists, or inhibitors with which they interact. Such structural analogs can be used to design drugs which are more active or stable forms of the polypeptide or which enhance or interfere with the function of a polypeptide in vivo. J. Hodgson, Bio/Technology 9:19-21 (1991).

For example, in one approach, the three-dimensional structure of a polypeptide, or of a polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of a polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous polypeptide-like molecules or to identify efficient inhibitors.

Useful examples of rational drug design may include molecules which have improved activity or stability as shown by S. Braxton et al., Biochemistry 31:7796-7801 (1992), or which act as inhibitors, agonists, or antagonists of

native peptides as shown by S.B.P. Athauda et al., J Biochem. (Tokyo) 113 (6):742-746 (1993).

It also is possible to isolate a target-specific antibody selected by an assay as described hereinabove, and then to determine its crystal structure. In principle this approach yields a pharmacophore upon which subsequent drug design can be based. It further is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies ("anti-ids") to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-id is an analog of the original receptor. The anti-id then can be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides then can act as the pharmacophore (that is, a prototype pharmaceutical drug).

A sufficient amount of a recombinant polypeptide of the present invention may be made available to perform analytical studies such as X-ray crystallography. In addition, knowledge of the polypeptide amino acid sequence which is derivable from the nucleic acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of, or in addition to, x-ray crystallography.

Antibodies specific to a BS200 polypeptide (e.g., anti-BS200 antibodies) further may be used to inhibit the biological action of the polypeptide by binding to the polypeptide. In this manner, the antibodies may be used in therapy, for example, to treat breast tissue diseases including breast cancer and its metastases.

Further, such antibodies can detect the presence or absence of a BS200 polypeptide in a test sample and, therefore, are useful as diagnostic markers for the diagnosis of a breast tissue disease or condition especially breast cancer. Such antibodies may also function as a diagnostic marker for breast tissue disease conditions, such as breast cancer.

The present invention also is directed to antagonists and inhibitors of the polypeptides of the present invention. The antagonists and inhibitors are those which inhibit or eliminate the function of the polypeptide. Thus, for example, an antagonist may bind to a polypeptide of the present invention and inhibit or eliminate its function. The antagonist, for example, could be an antibody against the polypeptide which eliminates the activity of a BS200 polypeptide by binding a BS200 polypeptide, or in some cases the antagonist may be an oligonucleotide.

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Examples of small molecule inhibitors include, but are not limited to, small peptides or peptide-like molecules.

The antagonists and inhibitors may be employed as a composition with a pharmaceutically acceptable carrier including, but not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof.

Administration of BS200 polypeptide inhibitors is preferably systemic. The present invention also provides an antibody which inhibits the action of such a polypeptide.

Antisense technology can be used to reduce gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes for the polypeptide of the present invention, is used to design an antisense RNA oligonucleotide of from 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription, thereby preventing transcription and the production of the BS200 polypeptide. For triple helix, see, for example, Lee et al., Nuc. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991). The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of a mRNA molecule into the BS200 polypeptide. For antisense, see, for example, Okano, J. Neurochem. 56:560 (1991); and "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression," CRC Press, Boca Raton, Fla. (1988). Antisense oligonucleotides act with greater efficacy when modified to contain artificial internucleotide linkages which render the molecule resistant to nucleolytic cleavage. Such artificial internucleotide linkages include, but are not limited to, methylphosphonate, phosphorothiolate and phosphoroamidate internucleotide linkages.

#### Recombinant Technology.

The present invention provides host cells and expression vectors comprising BS200 polynucleotides of the present invention and methods for the production of the polypeptide(s) they encode. Such methods comprise culturing the host cells under conditions suitable for the expression of the BS200 polynucleotide and recovering the BS200 polypeptide from the cell culture.

The present invention also provides vectors which include BS200 polynucleotides of the present invention, host cells which are genetically



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engineered with vectors of the present invention and the production of polypeptides of the present invention by recombinant techniques.

Host cells are genetically engineered (transfected, transduced or transformed) with the vectors of this invention which may be cloning vectors or expression vectors. The vector may be in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transfected cells, or amplifying BS200 gene(s). The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

The polynucleotides of the present invention may be employed for producing a polypeptide by recombinant techniques. Thus, the polynucleotide sequence may be included in any one of a variety of expression vehicles, in particular, vectors or plasmids for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus and pseudorabies. However, any other plasmid or vector may be used so long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into appropriate restriction endonuclease sites by procedures known in the art. Such procedures and others are deemed to be within the scope of those skilled in the art. The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. Representative examples of such promoters include, but are not limited to, the LTR or the SV40 promoter, the E. coli lac or trp, the phage lambda P sub L promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. In addition, the expression vectors preferably contain a gene to provide a phenotypic trait for selection of transfected host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in E. coli.

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The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transfect an appropriate host to permit the host to express the protein. As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as E. coli, Salmonella typhimurium; Streptomyces sp.; fungal cells, such as yeast; insect cells, such as Drosophila and Sf9; animal cells, such as CHO, COS or Bowes melanoma; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings provided herein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available. The following vectors are provided by way of example. Bacterial: pINCY (Incyte Pharmaceuticals Inc., Palo Alto, CA), pSPORT1 (Life Technologies, Gaithersburg, MD), pQE70, pQE60, pQE-9 (Qiagen) pBs, phagescript, psiX174, pBluescript SK, pBsKS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as it is replicable and viable in the host.

Plasmid pINCY is generally identical to the plasmid pSPORT1 (available from Life Technologies, Gaithersburg, MD) with the exception that it has two modifications in the polylinker (multiple cloning site). These modifications are (1) it lacks a HindIII restriction site and (2) its EcoRI restriction site lies at a different location. pINCY is created from pSPORT1 by cleaving pSPORT1 with both HindIII and EcoRI and replacing the excised fragment of the polylinker with synthetic DNA fragments (SEQUENCE ID NO 17 and SEQUENCE ID NO 18). This replacement may be made in any manner known to those of ordinary skill in the art. For example, the two nucleotide sequences, SEQUENCE ID NO 17 and SEQUENCE ID NO 18, may be generated synthetically with 5' terminal phosphates, mixed together, and then ligated under standard conditions for

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performing staggered end ligations into the pSPORT1 plasmid cut with HindIII and EcoRI. Suitable host cells (such as E. coli DH5 $\mu$  cells) then are transfected with the ligated DNA and recombinant clones are selected for ampicillin resistance. Plasmid DNA then is prepared from individual clones and subjected to restriction enzyme analysis or DNA sequencing in order to confirm the presence of insert sequences in the proper orientation. Other cloning strategies known to the ordinary artisan also may be employed.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, SP6, T7, gpt, lambda P sub R, P sub L and trp. Eukaryotic promoters include cytomegalovirus (CMV) immediate early, herpes simplex virus (HSV) thymidine kinase, early and late SV40, LTRs from retroviruses and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In a further embodiment, the present invention provides host cells containing the above-described construct. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (L. Davis et al., "Basic Methods in Molecular Biology," 2nd edition, Appleton and Lang, Paramount Publishing, East Norwalk, CT (1994)).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Recombinant proteins can be expressed in mammalian cells, yeast, bacteria, or other cells, under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook et al., Molecular Cloning: A Laboratory Manual, Second Edition, (Cold Spring Harbor, NY, 1989).

Transcription of a DNA encoding the polypeptide(s) of the present invention by higher eukaryotes is increased by inserting an enhancer sequence

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into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin (bp 100 to 270), a cytomegalovirus early promoter enhancer, a polyoma enhancer on the late side of the replication origin and adenovirus enhancers.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transfection of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transfection include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces* and *Staphylococcus*, although others may also be employed as a routine matter of choice.

Useful expression vectors for bacterial use comprise a selectable marker and bacterial origin of replication derived from plasmids comprising genetic elements of the well-known cloning vector pBR322 (ATCC 37017). Other vectors include but are not limited to PKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, WI). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

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Following transfection of a suitable host and growth of the host to an appropriate cell density, the selected promoter is derepressed by appropriate means (e.g., temperature shift or chemical induction), and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification. Microbial cells employed in expression of proteins can be disrupted by any convenient method including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well-known to the ordinary artisan.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts described by Gluzman, Cell 23:175 (1981), and other cell lines capable of expressing a compatible vector, such as the C127, HEK-293, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer and also any necessary ribosome binding sites, polyadenylation sites, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Representative, useful vectors include pRc/CMV and pcDNA3 (available from Invitrogen, San Diego, CA).

BS200 polypeptides are recovered and purified from recombinant cell cultures by known methods including affinity chromatography, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxyapatite chromatography or lectin chromatography. It is preferred to have low concentrations (approximately 0.1-5 mM) of calcium ion present during purification (Price, et al., J. Biol. Chem. 244:917 (1969)). Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

Thus, polypeptides of the present invention may be naturally purified products expressed from a high expressing cell line, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and

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mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated with mammalian or other eukaryotic carbohydrates or may be non-glycosylated. The polypeptides of the invention may also include an initial methionine amino acid residue.

The starting plasmids can be constructed from available plasmids in accord with published, known procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to one of ordinary skill in the art.

The following is the general procedure for the isolation and analysis of cDNA clones. In a particular embodiment disclosed herein, mRNA was isolated from breast tissue and used to generate the cDNA library. Breast tissue was obtained from patients by surgical resection and was classified as tumor or non-tumor tissue by a pathologist.

The cDNA inserts from random isolates of the breast tissue libraries were sequenced in part, analyzed in detail as set forth in the Examples, and are disclosed in the Sequence Listing as SEQUENCE ID NOS 1-14. Also analyzed in detail as set forth in the Examples, and disclosed in the Sequence Listing, is the full-length sequence of clone 3021177 (referred to as clone 3021177IH (SEQUENCE ID NO 15)). The consensus sequence of these inserts is presented as SEQUENCE ID NO 16. These polynucleotides may contain an entire open reading frame with or without associated regulatory sequences for a particular gene, or they may encode only a portion of the gene of interest. This is attributed to the fact that many genes are several hundred and sometimes several thousand bases in length and, with current technology, cannot be cloned in their entirety because of vector limitations, incomplete reverse transcription of the first strand, or incomplete replication of the second strand. Contiguous, secondary clones containing additional nucleotide sequences may be obtained using a variety of methods known to those of skill in the art.

Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ DNA polymerase, Klenow fragment, Sequenase (US Biochemical Corp, Cleveland, OH) or Taq polymerase to extend DNA chains from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. The chain termination reaction products may be electrophoresed on urea/polyacrylamide gels and detected either by

autoradiography (for radionucleotide labeled precursors) or by fluorescence (for fluorescent-labeled precursors). Recent improvements in mechanized reaction preparation, sequencing and analysis using the fluorescent detection method have permitted expansion in the number of sequences that can be determined per day using machines such as the Applied Biosystems 377 DNA Sequencers (Applied Biosystems, Foster City, CA).

The reading frame of the nucleotide sequence can be ascertained by several types of analyses. First, reading frames contained within the coding sequence can be analyzed for the presence of start codon ATG and stop codons TGA, TAA or TAG. Typically, one reading frame will continue throughout the major portion of a cDNA sequence while other reading frames tend to contain numerous stop codons. In such cases, reading frame determination is straightforward. In other more difficult cases, further analysis is required.

Algorithms have been created to analyze the occurrence of individual nucleotide bases at each putative codon triplet. See, for example J.W. Fickett, Nuc. Acids Res. 10:5303 (1982). Coding DNA for particular organisms (bacteria, plants and animals) tends to contain certain nucleotides within certain triplet periodicities, such as a significant preference for pyrimidines in the third codon position. These preferences have been incorporated into widely available software which can be used to determine coding potential (and frame) of a given stretch of DNA. The algorithm-derived information combined with start/stop codon information can be used to determine proper frame with a high degree of certainty. This, in turn, readily permits cloning of the sequence in the correct reading frame into appropriate expression vectors.

The nucleic acid sequences disclosed herein may be joined to a variety of other polynucleotide sequences and vectors of interest by means of well-established recombinant DNA techniques. See J. Sambrook et al., supra. Vectors of interest include cloning vectors, such as plasmids, cosmids, phage derivatives, phagemids, as well as sequencing, replication and expression vectors, and the like. In general, such vectors contain an origin of replication functional in at least one organism, convenient restriction endonuclease digestion sites and selectable markers appropriate for particular host cells. The vectors can be transferred by a variety of means known to those of skill in the art into suitable host cells which then produce the desired DNA, RNA or polypeptides.

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Occasionally, sequencing or random reverse transcription errors will mask the presence of the appropriate open reading frame or regulatory element. In such cases, it is possible to determine the correct reading frame by attempting to express the polypeptide and determining the amino acid sequence by standard peptide mapping and sequencing techniques. See, F.M. Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY (1989). Additionally, the actual reading frame of a given nucleotide sequence may be determined by transfection of host cells with vectors containing all three potential reading frames. Only those cells with the nucleotide sequence in the correct reading frame will produce a peptide of the predicted length.

The nucleotide sequences provided herein have been prepared by current, state-of-the-art, automated methods and, as such, may contain unidentified nucleotides. These will not present a problem to those skilled in the art who wish to practice the invention. Several methods employing standard recombinant techniques, described in J. Sambrook (supra) or periodic updates thereof, may be used to complete the missing sequence information. The same techniques used for obtaining a full length sequence, as described herein, may be used to obtain nucleotide sequences.

Expression of a particular cDNA may be accomplished by subcloning the cDNA into an appropriate expression vector and transfecting this vector into an appropriate expression host. The cloning vector used for the generation of the breast tissue cDNA library can be used for transcribing mRNA of a particular cDNA and contains a promoter for beta-galactosidase, an amino-terminal met and the subsequent seven amino acid residues of beta-galactosidase. Immediately following these eight residues is an engineered bacteriophage promoter useful for artificial priming and transcription, as well as a number of unique restriction sites, including EcoRI, for cloning. The vector can be transfected into an appropriate host strain of E. coli.

Induction of the isolated bacterial strain with isopropylthiogalactoside (IPTG) using standard methods will produce a fusion protein which contains the first seven residues of beta-galactosidase, about 15 residues of linker and the peptide encoded within the cDNA. Since cDNA clone inserts are generated by an essentially random process, there is one chance in three that the included cDNA will lie in the correct frame for proper translation. If the cDNA is not in the proper reading frame, the correct frame can be obtained by deletion or insertion of an appropriate number of bases by well known methods including in



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vitro mutagenesis, digestion with exonuclease III or mung bean nuclease, or oligonucleotide linker inclusion.

The cDNA can be shuttled into other vectors known to be useful for expression of protein in specific hosts. Oligonucleotide primers containing cloning sites and segments of DNA sufficient to hybridize to stretches at both ends of the target cDNA can be synthesized chemically by standard methods. These primers can then be used to amplify the desired gene segments by PCR. The resulting new gene segments can be digested with appropriate restriction enzymes under standard conditions and isolated by gel electrophoresis. Alternately, similar gene segments can be produced by digestion of the cDNA with appropriate restriction enzymes and filling in the missing gene segments with chemically synthesized oligonucleotides. Segments of the coding sequence from more than one gene can be ligated together and cloned in appropriate vectors to optimize expression of recombinant sequence.

Suitable expression hosts for such chimeric molecules include, but are not limited to, mammalian cells, such as Chinese Hamster Ovary (CHO) and human embryonic kidney (HEK) 293 cells, insect cells, such as Sf9 cells, yeast cells, such as Saccharomyces cerevisiae and bacteria, such as E. coli. For each of these cell systems, a useful expression vector may also include an origin of replication to allow propagation in bacteria and a selectable marker such as the beta-lactamase antibiotic resistance gene to allow selection in bacteria. In addition, the vectors may include a second selectable marker, such as the neomycin phosphotransferase gene, to allow selection in transfected eukaryotic host cells. Vectors for use in eukaryotic expression hosts may require the addition of 3' poly A tail if the sequence of interest lacks poly A.

Additionally, the vector may contain promoters or enhancers which increase gene expression. Such promoters are host specific and include, but are not limited to, MMTV, SV40, or metallothionine promoters for CHO cells; trp, lac, tac or T7 promoters for bacterial hosts; or alpha factor, alcohol oxidase or PGH promoters for yeast. Adenoviral vectors with or without transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to drive protein expression in mammalian cell lines. Once homogeneous cultures of recombinant cells are obtained, large quantities of recombinantly produced protein can be recovered from the conditioned medium and analyzed using chromatographic methods well known in the art. An alternative method for the production of large amounts of secreted protein involves the transfection of

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mammalian embryos and the recovery of the recombinant protein from milk produced by transgenic cows, goats, sheep, etc. Polypeptides and closely related molecules may be expressed recombinantly in such a way as to facilitate protein purification. One approach involves expression of a chimeric protein which includes one or more additional polypeptide domains not naturally present on human polypeptides. Such purification-facilitating domains include, but are not limited to, metal-chelating peptides such as histidine-tryptophan domains that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle, WA). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase from Invitrogen (San Diego, CA) between the polypeptide sequence and the purification domain may be useful for recovering the polypeptide.

#### Immunoassays.

BS200 polypeptides, including fragments, derivatives, and analogs thereof, or cells expressing such polypeptides, can be utilized in a variety of assays, many of which are described herein, for the detection of antibodies to breast tissue. They also can be used as immunogens to produce antibodies. These antibodies can be, for example, polyclonal or monoclonal antibodies, chimeric, single chain and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

For example, antibodies generated against a polypeptide comprising a sequence of the present invention can be obtained by direct injection of the polypeptide into an animal or by administering the polypeptide to an animal such as a mouse, rabbit, goat or human. A mouse, rabbit or goat is preferred. The polypeptide is selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. The antibody so obtained then will bind the polypeptide itself. In this manner, even a sequence encoding only a fragment of the polypeptide can be used to generate antibodies that bind the native polypeptide. Such antibodies then can be used to isolate the polypeptide from test samples such as tissue suspected of containing that polypeptide. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique as described by Kohler and Milstein, Nature 256:495-497

(1975), the trioma technique, the human B-cell hybridoma technique as described by Kozbor et al., Immun. Today 4:72 (1983) and the EBV-hybridoma technique to produce human monoclonal antibodies as described by Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc, New York, NY, pp. 77-96 (1985). Techniques described for the production of single chain antibodies can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention. See, for example, U.S. Patent No. 4,946,778.

Various assay formats may utilize the antibodies of the present invention, including "sandwich" immunoassays and probe assays. For example, the antibodies of the present invention, or fragments thereof, can be employed in various assay systems to determine the presence, if any, of BS200 antigen in a test sample. For example, in a first assay format, a polyclonal or monoclonal antibody or fragment thereof, or a combination of these antibodies, which has been coated on a solid phase, is contacted with a test sample, to form a first mixture. This first mixture is incubated for a time and under conditions sufficient to form antigen/antibody complexes. Then, an indicator reagent comprising a monoclonal or a polyclonal antibody or a fragment thereof, or a combination of these antibodies, to which a signal generating compound has been attached, is contacted with the antigen/antibody complexes to form a second mixture. This second mixture then is incubated for a time and under conditions sufficient to form antibody/antigen/antibody complexes. The presence of BS200 antigen in the test sample and captured on the solid phase, if any, is determined by detecting the measurable signal generated by the signal generating compound. The amount of BS200 antigen present in the test sample is proportional to the signal generated.

In an alternative assay format, a mixture is formed by contacting: (1) a polyclonal antibody, monoclonal antibody, or fragment thereof, which specifically binds to BS200 antigen, or a combination of such antibodies bound to a solid support; (2) the test sample; and (3) an indicator reagent comprising a monoclonal antibody, polyclonal antibody, or fragment thereof, which specifically binds to a different BS200 antigen (or a combination of these antibodies) to which a signal generating compound is attached. This mixture is incubated for a time and under conditions sufficient to form antibody/antigen/antibody complexes. The presence, if any, of BS200 antigen present in the test sample and captured on the solid phase is determined by

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detecting the measurable signal generated by the signal generating compound. The amount of BS200 antigen present in the test sample is proportional to the signal generated.

In another assay format, one or a combination of at least two monoclonal antibodies of the invention can be employed as a competitive probe for the detection of antibodies to BS200 antigen. For example, BS200 polypeptides such as the recombinant antigens disclosed herein, either alone or in combination, are coated on a solid phase. A test sample suspected of containing antibody to BS200 antigen then is incubated with an indicator reagent comprising a signal generating compound and at least one monoclonal antibody of the invention for a time and under conditions sufficient to form antigen/antibody complexes of either the test sample and indicator reagent bound to the solid phase or the indicator reagent bound to the solid phase. The reduction in binding of the monoclonal antibody to the solid phase can be quantitatively measured.

In yet another detection method, each of the monoclonal or polyclonal antibodies of the present invention can be employed in the detection of BS200 antigens in tissue sections, as well as in cells, by immunohistochemical analysis. The tissue sections can be cut from either frozen or chemically fixed samples of tissue. If the antigens are to be detected in cells, the cells can be isolated from blood, urine, breast aspirates, or other bodily fluids. The cells may be obtained by biopsy, either surgical or by needle. The cells can be isolated by centrifugation or magnetic attraction after labeling with magnetic particles or ferrofluids so as to enrich a particular fraction of cells for staining with the antibodies of the present invention. Cytochemical analysis wherein these antibodies are labeled directly (with, for example, fluorescein, colloidal gold, horseradish peroxidase, alkaline phosphatase, etc.) or are labeled by using secondary labeled anti-species antibodies (with various labels as exemplified herein) to track the histopathology of disease also are within the scope of the present invention.

In addition, these monoclonal antibodies can be bound to matrices similar to CNBr-activated Sepharose and used for the affinity purification of specific BS200 polypeptides from cell cultures or biological tissues such as to purify recombinant and native BS200 proteins.

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The monoclonal antibodies of the invention also can be used for the generation of chimeric antibodies for therapeutic use, or other similar applications.

The monoclonal antibodies or fragments thereof can be provided individually to detect BS200 antigens. Combinations of the monoclonal antibodies (and fragments thereof) provided herein also may be used together as components in a mixture or "cocktail" of at least one BS200 antibody of the invention, along with antibodies which specifically bind to other BS200 regions, each antibody having different binding specificities. Thus, this cocktail can include the monoclonal antibodies of the invention which are directed to BS200 polypeptides disclosed herein and other monoclonal antibodies specific to other antigenic determinants of BS200 antigens or other related proteins.

The polyclonal antibody or fragment thereof which can be used in the assay formats should specifically bind to a BS200 polypeptide or other BS200 polypeptides additionally used in the assay. The polyclonal antibody used preferably is of mammalian origin such as, human, goat, rabbit or sheep polyclonal antibody which binds BS200 polypeptide. Most preferably, the polyclonal antibody is of rabbit origin. The polyclonal antibodies used in the assays can be used either alone or as a cocktail of polyclonal antibodies. Since the cocktails used in the assay formats are comprised of either monoclonal antibodies or polyclonal antibodies having different binding specificity to BS200 polypeptides, they are useful for the detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases and conditions of the breast, such as breast cancer.

It is contemplated and within the scope of the present invention that BS200 antigen may be detectable in assays by use of a recombinant antigen as well as by use of a synthetic peptide or purified peptide, which peptide comprises an amino acid sequence of BS200. The amino acid sequence of such a polypeptide is selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. It also is within the scope of the present invention that different synthetic, recombinant or purified peptides, identifying different epitopes of BS200, can be used in combination in an assay for the detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to diseases and conditions of the breast, such as breast cancer. In this case, all of these peptides can be coated

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onto one solid phase; or each separate peptide may be coated onto separate solid phases, such as microparticles, and then combined to form a mixture of peptides which can be later used in assays. Furthermore, it is contemplated that multiple peptides which define epitopes from different antigens may be used for the detection, diagnosis, staging, monitoring, prognosis, prevention or treatment of, or determining the predisposition to, diseases and conditions of the breast, such as breast cancer. Peptides coated on solid phases or labeled with detectable labels are then allowed to compete with those present in a patient sample (if any) for a limited amount of antibody. A reduction in binding of the synthetic, recombinant, or purified peptides to the antibody (or antibodies) is an indication of the presence of BS200 antigen in the patient sample. The presence of BS200 antigen indicates the presence of breast tissue disease, especially breast cancer, in the patient. Variations of assay formats are known to those of ordinary skill in the art and many are discussed herein below.

In another assay format, the presence of anti-BS200 antibody and/or BS200 antigen can be detected in a simultaneous assay, as follows. A test sample is simultaneously contacted with a capture reagent of a first analyte, wherein said capture reagent comprises a first binding member specific for a first analyte attached to a solid phase and a capture reagent for a second analyte, wherein said capture reagent comprises a first binding member for a second analyte attached to a second solid phase, to thereby form a mixture. This mixture is incubated for a time and under conditions sufficient to form capture reagent/first analyte and capture reagent/second analyte complexes. These so-formed complexes then are contacted with an indicator reagent comprising a member of a binding pair specific for the first analyte labeled with a signal generating compound and an indicator reagent comprising a member of a binding pair specific for the second analyte labeled with a signal generating compound to form a second mixture. This second mixture is incubated for a time and under conditions sufficient to form capture reagent/first analyte/indicator reagent complexes and capture reagent/second analyte/indicator reagent complexes. The presence of one or more analytes is determined by detecting a signal generated in connection with the complexes formed on either or both solid phases as an indication of the presence of one or more analytes in the test sample. In this assay format, recombinant antigens derived from the expression systems disclosed herein may be utilized, as well as monoclonal antibodies produced from the proteins derived from the expression systems as

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disclosed herein. For example, in this assay system, BS200 antigen can be the first analyte. Such assay systems are described in greater detail in EP Publication No. 0473065.

In yet other assay formats, the polypeptides disclosed herein may be utilized to detect the presence of antibody against BS200 antigen in test samples. For example, a test sample is incubated with a solid phase to which at least one polypeptide such as a recombinant protein or synthetic peptide has been attached. The polypeptide is selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. These are reacted for a time and under conditions sufficient to form antigen/antibody complexes. Following incubation, the antigen/antibody complex is detected. Indicator reagents may be used to facilitate detection, depending upon the assay system chosen. In another assay format, a test sample is contacted with a solid phase to which a recombinant protein produced as described herein is attached, and also is contacted with a monoclonal or polyclonal antibody specific for the protein, which preferably has been labeled with an indicator reagent. After incubation for a time and under conditions sufficient for antibody/antigen complexes to form, the solid phase is separated from the free phase, and the label is detected in either the solid or free phase as an indication of the presence of antibody against BS200 antigen. Other assay formats utilizing the recombinant antigens disclosed herein are contemplated. These include contacting a test sample with a solid phase to which at least one antigen from a first source has been attached, incubating the solid phase and test sample for a time and under conditions sufficient to form antigen/antibody complexes, and then contacting the solid phase with a labeled antigen, which antigen is derived from a second source different from the first source. For example, a recombinant protein derived from a first source such as E. coli is used as a capture antigen on a solid phase, a test sample is added to the so-prepared solid phase, and following standard incubation and washing steps as deemed or required, a recombinant protein derived from a different source (i.e., non-E. coli) is utilized as a part of an indicator reagent which subsequently is detected. Likewise, combinations of a recombinant antigen on a solid phase and synthetic peptide in the indicator phase also are possible. Any assay format which utilizes an antigen specific for BS200 produced or derived from a first source as the capture antigen and an antigen specific for BS200 from a different second source is contemplated. Thus,

various combinations of recombinant antigens, as well as the use of synthetic peptides, purified proteins and the like, are within the scope of this invention. Assays such as this and others are described in U.S. Patent No. 5,254,458, which enjoys common ownership herewith.

Other embodiments which utilize various other solid phases also are contemplated and are within the scope of this invention. For example, ion capture procedures for immobilizing an immobilizable reaction complex with a negatively charged polymer (described in EP publication 0326100 and EP publication No. 0406473), can be employed according to the present invention to effect a fast solution-phase immunochemical reaction. An immobilizable immune complex is separated from the rest of the reaction mixture by ionic interactions between the negatively charged poly-anion/immune complex and the previously treated, positively charged porous matrix and detected by using various signal generating systems previously described, including those described in chemiluminescent signal measurements as described in EPO Publication No. 0 273,115.

Also, the methods of the present invention can be adapted for use in systems which utilize microparticle technology including automated and semi-automated systems wherein the solid phase comprises a microparticle (magnetic or non-magnetic). Such systems include those described in, for example, published EPO applications Nos. EP 0 425 633 and EP 0 424 634, respectively.

The use of scanning probe microscopy (SPM) for immunoassays also is a technology to which the monoclonal antibodies of the present invention are easily adaptable. In scanning probe microscopy, particularly in atomic force microscopy, the capture phase, for example, at least one of the monoclonal antibodies of the invention, is adhered to a solid phase and a scanning probe microscope is utilized to detect antigen/antibody complexes which may be present on the surface of the solid phase. The use of scanning tunneling microscopy eliminates the need for labels which normally must be utilized in many immunoassay systems to detect antigen/antibody complexes. The use of SPM to monitor specific binding reactions can occur in many ways. In one embodiment, one member of a specific binding partner (analyte specific substance which is the monoclonal antibody of the invention) is attached to a surface suitable for scanning. The attachment of the analyte specific substance may be by adsorption to a test piece which comprises a solid phase of a plastic or metal surface, following methods known to those of ordinary skill in the art. Or,



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covalent attachment of a specific binding partner (analyte specific substance) to a test piece which test piece comprises a solid phase of derivatized plastic, metal, silicon, or glass may be utilized. Covalent attachment methods are known to those skilled in the art and include a variety of means to irreversibly link specific binding partners to the test piece. If the test piece is silicon or glass, the surface must be activated prior to attaching the specific binding partner. Also, polyelectrolyte interactions may be used to immobilize a specific binding partner on a surface of a test piece by using techniques and chemistries. The preferred method of attachment is by covalent means. Following attachment of a specific binding member, the surface may be further treated with materials such as serum, proteins, or other blocking agents to minimize non-specific binding. The surface also may be scanned either at the site of manufacture or point of use to verify its suitability for assay purposes. The scanning process is not anticipated to alter the specific binding properties of the test piece.

While the present invention discloses the preference for the use of solid phases, it is contemplated that the reagents such as antibodies, proteins and peptides of the present invention can be utilized in non-solid phase assay systems. These assay systems are known to those skilled in the art, and are considered to be within the scope of the present invention.

It is contemplated that the reagent employed for the assay can be provided in the form of a test kit with one or more containers such as vials or bottles, with each container containing a separate reagent such as a probe, primer, monoclonal antibody or a cocktail of monoclonal antibodies, or a polypeptide (e.g. recombinantly, synthetically produced or purified) employed in the assay. The polypeptide is selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof. Other components such as buffers, controls and the like, known to those of ordinary skill in art, may be included in such test kits. It also is contemplated to provide test kits which have means for collecting test samples comprising accessible body fluids, e.g., blood, urine, saliva and stool. Such tools useful for collection ("collection materials") include lancets and absorbent paper or cloth for collecting and stabilizing blood; swabs for collecting and stabilizing saliva; cups for collecting and stabilizing urine or stool samples. Collection materials, papers, cloths, swabs, cups and the like, may optionally be treated to avoid denaturation or irreversible adsorption of the sample. The collection materials also may be treated with or contain

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preservatives, stabilizers or antimicrobial agents to help maintain the integrity of the specimens. Test kits designed for the collection, stabilization and preservation of test specimens obtained by surgery or needle biopsy are also useful. It is contemplated that all kits may be configured in two components which can be provided separately; one component for collection and transport of the specimen and the other component for the analysis of the specimen. The collection component, for example, can be provided to the open market user while the components for analysis can be provided to others such as laboratory personnel for determination of the presence, absence or amount of analyte. Further, kits for the collection, stabilization and preservation of test specimens may be configured for use by untrained personnel and may be available in the open market for use at home with subsequent transportation to a laboratory for analysis of the test sample.

#### In Vivo Antibody Use.

Antibodies of the present invention can be used in vivo; that is, they can be injected into patients suspected of having or having diseases of the breast for diagnostic or therapeutic uses. The use of antibodies for in vivo diagnosis is well known in the art. Sumerdon et al, Nucl. Med. Biol. 17:247-254 (1990) have described an optimized antibody-chelator for the radioimmunosintographic imaging of carcinoembryonic antigen (CEA) expressing tumors using Indium-111 as the label. Griffin et al, J. Clin. Onc. 9:631-640 (1991) have described the use of this agent in detecting tumors in patients suspected of having recurrent colorectal cancer. The use of similar agents with paramagnetic ions as labels for magnetic resonance imaging is known in the art (R. B. Lauffer, Magnetic Resonance in Medicine 22:339-342 (1991)). It is anticipated that antibodies directed against BS200 antigen can be injected into patients suspected of having a disease of the breast such as breast cancer for the purpose of diagnosing or staging the disease status of the patient. The label used will depend on the imaging modality chosen. Radioactive labels such as Indium-111, Technetium-99m, or Iodine-131 can be used for planar scans or single photon emission computed tomography (SPECT). Positron emitting labels such as Fluorine-19 can also be used for positron emission tomography (PET). For MRI, paramagnetic ions such as Gadolinium (III) or Manganese (II) can be used. Localization of the label within the breast or external to the breast may allow determination of spread of the disease. The amount of label within the breast may allow determination of the presence or absence of cancer of the breast.

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For patients known to have a disease of the breast, injection of an antibody directed against BS200 antigen may have therapeutic benefit. The antibody may exert its effect without the use of attached agents by binding to BS200 antigen expressed on or in the tissue or organ. Alternatively, the antibody may be conjugated to cytotoxic agents such as drugs, toxins, or radionuclides to enhance its therapeutic effect. Garnett and Baldwin, Cancer Research 46:2407-2412 (1986) have described the preparation of a drug-mono-clonal antibody conjugate. Pastan et al, Cell 47:641-648 (1986) have reviewed the use of toxins conjugated to monoclonal antibodies for the therapy of various cancers. Goodwin and Meares, Cancer Supplement 80:2675-2680 (1997) have described the use of Yttrium-90 labeled monoclonal antibodies in various strategies to maximize the dose to tumor while limiting normal tissue toxicity. Other known cytotoxic radionuclides include Copper-67, Iodine-131, and Rhenium-186 all of which can be used to label monoclonal antibodies directed against BS200 antigen for the treatment of cancer of the breast.

E. coli bacteria (clone 3021177) was deposited on November 4, 1997 with the American Type Culture Collection (A.T.C.C.), 12301 Parklawn Drive, Rockville, Maryland 20852. The deposit was made under the terms of the Budapest Treaty and will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the last request for the deposit, or for the enforceable period of the U.S. patent, whichever is longer. The deposit and any other deposited material described herein are provided for convenience only, and are not required to practice the present invention in view of the teachings provided herein. The cDNA sequence in all of the deposited material is incorporated herein by reference. Clone 3021177 was accorded A.T.C.C. Deposit No. 98573.

The present invention will now be described by way of examples, which are meant to illustrate, but not to limit, the scope of the present invention.

### EXAMPLES

#### Example 1: Identification of Breast Tissue Library BS200 Gene-Specific Clones

A. Library Comparison of Expressed Sequence Tags (EST's) or Transcript Images. Partial sequences of cDNA clone inserts, so-called "expressed sequence tags" (EST's), were derived from cDNA libraries made from breast tumor tissues, breast non-tumor tissues and numerous other tissues, both tumor and non-tumor and entered into a database (LIFESEQ™ database,

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available from Incyte Pharmaceuticals, Palo Alto, CA) as gene transcript images. See International Publication No. WO 95/20681. (A transcript image is a listing of the number of EST's for each of the represented genes in a given tissue library. EST's sharing regions of mutual sequence overlap are classified into clusters. A cluster is assigned a clone number from a representative 5' EST. Often, a cluster of interest can be extended by comparing its consensus sequence with sequences of other EST's which did not meet the criteria for automated clustering. The alignment of all available clusters and single EST's represent a contig from which a consensus sequence is derived.) The transcript images then were evaluated to identify EST sequences that were representative primarily of the breast tissue libraries. These target clones then were ranked according to their abundance (occurrence) in the target libraries and their absence from background libraries. Higher abundance clones with low background occurrence were given higher study priority. EST's corresponding to the consensus sequence of BS200 were found in 38.8% (7 of 18) of breast tissue libraries. EST's corresponding to the consensus sequence SEQUENCE ID NO 16 (or fragments thereof) were found in only 5.0% (18 of 355) of the other, non-breast, libraries of the data base. Therefore, the consensus sequence or fragment thereof was found more than 7 times more often in breast than non-breast tissues. Overlapping clones 2767006 (SEQUENCE ID NO 1), 3021177 (SEQUENCE ID NO 2), 3213801 (SEQUENCE ID NO 3), 2224165 (SEQUENCE ID NO 4), 1316156 (SEQUENCE ID NO 5), 1549512 (SEQUENCE ID NO 6), 1919065 (SEQUENCE ID NO 7), g898160 (SEQUENCE ID NO 8), 2116945 (SEQUENCE ID NO 9), g1985883 (SEQUENCE ID NO 10), 1925574 (SEQUENCE ID NO 11), 3724828 (SEQUENCE ID NO 12), g1444044 (SEQUENCE ID NO 13), and 1808382 (SEQUENCE ID NO 14), respectively, were identified for further study. These represented the minimum number of clones that, along with the full-length sequence of clone 3021177 (hereinafter referred to as "clone 3021177IH (SEQUENCE ID NO 15)"), were needed to form the contig and from which the consensus sequence provided herein (SEQUENCE ID NO 16) was derived.

B. Generation of a Consensus Sequence. The nucleotide sequences of clones 2767006 (SEQUENCE ID NO 1), 3021177 (SEQUENCE ID NO 2), 3213801 (SEQUENCE ID NO 3), 2224165 (SEQUENCE ID NO 4), 1316156 (SEQUENCE ID NO 5), 1549512 (SEQUENCE ID NO 6), 1919065 (SEQUENCE ID NO 7), g898160 (SEQUENCE ID NO 8), 2116945

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(SEQUENCE ID NO 9), g1985883 (SEQUENCE ID NO 10), 1925574 (SEQUENCE ID NO 11), 3724828 (SEQUENCE ID NO 12), g1444044 (SEQUENCE ID NO 13), 1808382 (SEQUENCE ID NO 14), and 3021177IH (SEQUENCE ID NO 15) were entered in the Sequencher™ Program (available from Gene Codes Corporation, Ann Arbor, MI) in order to generate a nucleotide alignment (contig map) and then generate their consensus sequence (SEQUENCE ID NO 16). Figures 1A-1E show the nucleotide sequence alignment of these clones and their resultant nucleotide consensus sequence (SEQUENCE ID NO 16). Figure 2 presents the contig map depicting the clones 2767006 (SEQUENCE ID NO 1), 3021177 (SEQUENCE ID NO 2), 3213801 (SEQUENCE ID NO 3), 2224165 (SEQUENCE ID NO 4), 1316156 (SEQUENCE ID NO 5), 1549512 (SEQUENCE ID NO 6), 1919065 (SEQUENCE ID NO 7), g898160 (SEQUENCE ID NO 8), 2116945 (SEQUENCE ID NO 9), g1985883 (SEQUENCE ID NO 10), 1925574 (SEQUENCE ID NO 11), 3724828 (SEQUENCE ID NO 12), g1444044 (SEQUENCE ID NO 13), 1808382 (SEQUENCE ID NO 14 and 3021177IH (SEQUENCE ID NO 15), which form overlapping regions of the BS200 gene, and the resultant consensus nucleotide sequence (SEQUENCE ID NO 16) of these clones in a graphic display. Following this, a three-frame translation was performed on the consensus sequence (SEQUENCE ID NO 16). The first forward frame was found to have an open reading frame encoding a 516 residue amino acid sequence which is presented as SEQUENCE ID NO 31. The open reading frame corresponds to nucleotides 1-1548 of SEQUENCE ID NO 16.

Analysis of the LIFESEQ™ database indicates a possible T/C polymorphism at position 323 in the consensus nucleotide sequence (SEQUENCE ID NO 16). Three occurrences of the T nucleotide variant and two occurrences of the C nucleotide variant were noted in the database. This polymorphism at nucleotide 323 results in an amino acid shift between methionine (ATG) and threonine (ACG).

#### Example 2: Sequencing of BS200 EST-Specific Clones

The full-length DNA sequence of clone 3021177 of the BS200 gene contig was determined (clone 3021177IH, SEQUENCE ID NO 15) using dideoxy termination sequencing with dye terminators following known methods [F. Sanger et al., PNAS U.S.A. 74:5463 (1977)].

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Because vectors such as pSPORT1 (Life Technologies, Gaithersburg, MD) and pINCY (available from Incyte Pharmaceuticals, Inc., Palo Alto, CA) contain universal priming sites just adjacent to the 3' and 5' ligation junctions of the inserts, the inserts were sequenced in both directions using two universal primers (SEQUENCE ID NO 19 and SEQUENCE ID NO 20, available from New England Biolabs, Beverly, MA, and Applied Biosystems Inc, Foster City, CA, respectively). The sequencing reactions were run on a polyacrylamide denaturing gel, and the sequences were determined by an Applied Biosystems 377 Sequencer (available from Applied Biosystems, Foster City, CA). Additional sequencing primers (SEQUENCE ID NOS 21-28) were designed from sequence information of the consensus sequence (SEQUENCE ID NO 16). These primers then were used to determine the remaining DNA sequence of the cloned insert from each DNA strand, as previously described.

#### Example 3: Nucleic Acid

A. RNA Extraction from Tissue. Total RNA was isolated from breast tissues and from non-breast tissues. Various methods were utilized, including but not limited to the lithium chloride/urea technique, known in the art and described by Kato et al., (*J. Virol.* 61:2182-2191, 1987), and TRIzol™ (Gibco-BRL, Grand Island, NY).

Briefly, tissue was placed in a sterile conical tube on ice and 10-15 volumes of 3 M LiCl, 6 M urea, 5 mM EDTA, 0.1 M  $\beta$ -mercaptoethanol, 50 mM Tris-HCl (pH 7.5) were added. The tissue is homogenized with a Polytron® homogenizer (Brinkman Instruments, Inc., Westbury, NY) for 30-50 sec on ice. The solution was transferred to a 15 ml plastic centrifuge tube and placed overnight at -20°C. The tube was centrifuged for 90 min at 9,000 x g at 0-4°C and the supernatant was immediately decanted. Ten ml of 3 M LiCl were added and the tube was vortexed for 5 sec. The tube was centrifuged for 45 min at 11,000 x g at 0-4°C. The decanting, resuspension in LiCl, and centrifugation was repeated and the final pellet was air dried and suspended in 2 ml of 1 mM EDTA, 0.5% SDS, 10 mM Tris (pH 7.5). Twenty microliters (20  $\mu$ l) of Proteinase K (20 mg/ml) were added, and the solution was incubated for 30 min at 37°C with occasional mixing. One-tenth volume (0.22-0.25 ml) of 3 M NaCl was added and the solution was vortexed before transfer into another tube containing 2 ml of phenol/chloroform/isoamyl alcohol (PCI). The tube was vortexed for 1-3 sec and centrifuged for 20 min at 3,000 x g at 10°C. The PCI

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extraction was repeated and followed by two similar extractions with chloroform/isoamyl alcohol (CI). The final aqueous solution was transferred to a prechilled 15 ml Corex glass tube containing 6 ml of absolute ethanol, the tube was covered with parafilm, and placed at -20°C overnight. The tube was centrifuged for 30 min at 10,000 x g at 0-4°C and the ethanol supernatant was decanted immediately. The RNA pellet was washed four times with 10 ml of 75% ice-cold ethanol and the final pellet was air dried for 15 min at room temperature. The RNA was suspended in 0.5 ml of 10 mM TE (pH 7.6, 1 mM EDTA) and its concentration was determined spectrophotometrically. RNA samples were aliquoted and stored at -70°C as ethanol precipitates.

The quality of the RNA is determined by agarose gel electrophoresis (see Example 5, Northern Blot Analysis) and staining with 0.5 µg/ml ethidium bromide for one hour. RNA samples that do not contain intact rRNAs are excluded from the study.

Alternatively, for RT-PCR analysis, 1 ml of Ultraspec RNA reagent was added to 120 mg of pulverized tissue in a 2.0 ml polypropylene microfuge tube, homogenized with a Polytron® homogenizer (Brinkman Instruments, Inc., Westbury, NY) for 50 sec and placed on ice for 5 min. Then, 0.2 ml of chloroform was added to each sample, followed by vortexing for 15 sec. The sample was placed on ice for another 5 min, followed by centrifugation at 12,000 x g for 15 min at 4°C. The upper layer was collected and transferred to another RNase-free 2.0 ml microfuge tube. An equal volume of isopropanol was added to each sample, and the solution was placed on ice for 10 min. The sample was centrifuged at 12,000 x g for 10 min at 4°C, and the supernatant was discarded. The remaining pellet was washed twice with cold 75% ethanol, resuspended by vortexing, and the resuspended material was then pelleted by centrifugation at 7500 x g for 5 min at 4°C. Finally, the RNA pellet was dried in a Speedvac (Savant, Farmingdale, NY) for 5 min and reconstituted in RNase-free water.

B. RNA Extraction from Blood Mononuclear Cells. Mononuclear cells are isolated from blood samples from patients by centrifugation using Ficoll-Hypaque as follows. A 10 ml volume of whole blood is mixed with an equal volume of RPMI Medium (Gibco-BRL, Grand Island, NY). This mixture is then underlayered with 10 ml of Ficoll-Hypaque (Pharmacia, Piscataway, NJ) and centrifuged for 30 minutes at 200 x g. The buffy coat containing the mononuclear cells is removed, diluted to 50 ml with Dulbecco's PBS (Gibco-BRL, Grand Island, NY) and the mixture centrifuged for 10 minutes at 200 x g.

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After two washes, the resulting pellet is resuspended in Dulbecco's PBS to a final volume of 1 ml.

RNA is prepared from the isolated mononuclear cells as described by N. Kato et al., J. Virology 61:2182-2191 (1987). Briefly, the pelleted mononuclear cells are brought to a final volume of 1 ml and then are resuspended in 250  $\mu$ L of PBS and mixed with 2.5 ml of 3 M LiCl, 6 M urea, 5 mM EDTA, 0.1 M 2-mercaptoethanol, 50 mM Tris-HCl (pH 7.5). The resulting mixture is homogenized and incubated at -20°C overnight. The homogenate is centrifuged at 8,000 RPM in a Beckman J2-21M rotor for 90 minutes at 0-4°C. The pellet is resuspended in 10 ml of 3 M LiCl by vortexing and then centrifuged at 10,000 RPM in a Beckman J2-21M rotor centrifuge for 45 minutes at 0-4°C. The resuspending and pelleting steps then are repeated. The pellet is resuspended in 2 ml of 1 mM EDTA, 0.5% SDS, 10 mM Tris (pH 7.5) and 400  $\mu$ g Proteinase K with vortexing and then it is incubated at 37°C for 30 minutes with shaking. One tenth volume of 3 M NaCl then is added and the mixture is vortexed. Proteins are removed by two cycles of extraction with phenol/ chloroform/ isoamyl alcohol (PCI) followed by one extraction with chloroform/ isoamyl alcohol (CI). RNA is precipitated by the addition of 6 ml of absolute ethanol followed by overnight incubation at -20°C. After the precipitated RNA is collected by centrifugation, the pellet is washed 4 times in 75% ethanol. The pelleted RNA is then dissolved in solution containing 1 mM EDTA, 10 mM Tris-HCl (pH 7.5).

Non-breast tissues are used as negative controls. The mRNA can be further purified from total RNA by using commercially available kits such as oligo dT cellulose spin columns (RediCol™ from Pharmacia, Uppsala, Sweden) for the isolation of poly-adenylated RNA. Total RNA or mRNA can be dissolved in lysis buffer (5 M guanidine thiocyanate, 0.1 M EDTA, pH 7.0) for analysis in the ribonuclease protection assay.

C. RNA Extraction from polysomes. Tissue is minced in saline at 4°C and mixed with 2.5 volumes of 0.8 M sucrose in a TK<sub>150</sub>M (150 mM KCl, 5 mM MgCl<sub>2</sub>, 50 mM Tris-HCl, pH 7.4) solution containing 6 mM 2-mercaptoethanol. The tissue is homogenized in a Teflon-glass Potter homogenizer with five strokes at 100-200 rpm followed by six strokes in a Dounce homogenizer, as described by B. Mechler, Methods in Enzymology 152:241-248 (1987). The homogenate then is centrifuged at 12,000 x g for 15 min at 4°C to sediment the nuclei. The polysomes are isolated by mixing 2 ml of the supernatant with 6 ml



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of 2.5 M sucrose in TK<sub>150</sub>M and layering this mixture over 4 ml of 2.5 M sucrose in TK<sub>150</sub>M in a 38 ml polyallomer tube. Two additional sucrose TK<sub>150</sub>M solutions are successively layered onto the extract fraction; a first layer of 13 ml 2.05 M sucrose followed by a second layer of 6 ml of 1.3 M sucrose. The polysomes are isolated by centrifuging the gradient at 90,000 x g for 5 hr at 4°C. The fraction then is taken from the 1.3 M sucrose/2.05 M sucrose interface with a siliconized pasteur pipette and diluted in an equal volume of TE (10 mM Tris-HCl, pH 7.4, 1 mM EDTA). An equal volume of 90°C SDS buffer (1% SDS, 200 mM NaCl, 20 mM Tris-HCl, pH 7.4) is added and the solution is incubated in a boiling water bath for 2 min. Proteins next are digested with a Proteinase K digestion (50 mg/ml) for 15 min at 37°C. The mRNA is purified with 3 equal volumes of phenol-chloroform extractions followed by precipitation with 0.1 volume of 2 M sodium acetate (pH 5.2) and 2 volumes of 100% ethanol at -20°C overnight. The precipitated RNA is recovered by centrifugation at 12,000 x g for 10 min at 4°C. The RNA is dried and resuspended in TE (pH 7.4) or distilled water. The resuspended RNA then can be used in a slot blot or dot blot hybridization assay to check for the presence of BS200 mRNA (see Example 6).

The quality of nucleic acid and proteins is dependent on the method of preparation used. Each sample may require a different preparation technique to maximize isolation efficiency of the target molecule. These preparation techniques are within the skill of the ordinary artisan.

#### Example 4: Ribonuclease Protection Assay

##### A. Synthesis of Labeled Complementary RNA (cRNA) Hybridization

Probe and Unlabeled Sense Strand. Labeled antisense and unlabeled sense riboprobes are transcribed from the BS200 gene cDNA sequence which contains a 5' RNA polymerase promoter such as SP6 or T7. The sequence may be from a vector containing the appropriate BS200 cDNA insert, or from a PCR-generated product of the insert using PCR primers which incorporate a 5' RNA polymerase promoter sequence. For example, the described plasmid, clone 3021177 or another comparable clone, containing the BS200 gene cDNA sequence, flanked by opposed SP6 and T7 or other RNA polymerase promoters, is purified using a Qiagen Plasmid Purification Kit (Qiagen, Chatsworth, CA). Then 10 µg of the plasmid DNA are linearized by cutting with an appropriate restriction enzyme such as DdeI for 1 hr at 37°C. The linearized plasmid DNA is purified using the QIAprep Kit (Qiagen, Chatsworth, CA) and used for the synthesis of antisense

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transcript from the appropriate promoter using the Riboprobe<sup>®</sup> in vitro Transcription System (Promega Corporation, Madison, WI), as described by the supplier's instructions, incorporating either (alpha-<sup>32</sup>P) CTP (Amersham Life Sciences, Inc. Arlington Heights, IL) or biotinylated CTP as a label. To generate the sense strand, 10 µg of the purified plasmid DNA are cut with restriction enzymes, such as XbaI and NotI, and transcribed as above from the appropriate promoter. Both sense and antisense strands are isolated by spin column chromatography. Unlabeled sense strand is quantitated by UV absorption at 260 nm.

B. Hybridization of Labeled Probe to Target. Frozen tissue is pulverized to powder under liquid nitrogen and 100-500 mg are dissolved in 1 ml of lysis buffer, available as a component of the Direct Protect<sup>™</sup> Lysate RNase Protection Kit (Ambion, Inc., Austin, TX). Further dissolution can be achieved using a tissue homogenizer. In addition, a dilution series of a known amount of sense strand in mouse liver lysate is made for use as a positive control. Finally, 45 µl of solubilized tissue or diluted sense strand is mixed directly with either: (1)  $1 \times 10^5$  cpm of radioactively labeled probe; or (2) 250 pg of non-isotopically labeled probe in 5 µl of lysis buffer. Hybridization is allowed to proceed overnight at 37°C. See, T. Kaabache et al., Anal. Biochem. 232:225-230 (1995).

C. RNase Digestion. RNA that is not hybridized to probe is removed from the reaction as per the Direct Protect<sup>™</sup> protocol using a solution of RNase A and RNase T1 for 30 min at 37°C, followed by removal of RNase by Proteinase K digestion in the presence of sodium sarcosyl. Hybridized fragments protected from digestion are then precipitated by the addition of an equal volume of isopropanol and placed at -70°C for 3 hr. The precipitates are collected by centrifugation at 12,000 x g for 20 min.

D. Fragment Analysis. The precipitates are dissolved in denaturing gel loading dye (80% formamide, 10 mM EDTA (pH 8.0), 1 mg/ml xylene cyanol, 1 mg/ml bromophenol blue), heat denatured, and electrophoresed in 6% polyacrylamide TBE, 8 M urea denaturing gels. The gels are imaged and analyzed using the STORM<sup>™</sup> storage phosphor autoradiography system (Molecular Dynamics, Sunnyvale, CA). Quantitation of protected fragment bands, expressed in femtograms (fg), is achieved by comparing the peak areas obtained from the test samples to those from the known dilutions of the positive control sense strand (see Section B, supra). The results are expressed in molecules of BS200 RNA/cell and as a image rating score. In cases where non-

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isotopic labels are used, hybrids are transferred from the gels to membranes (nylon or nitrocellulose) by blotting and then analyzed using detection systems that employ streptavidin alkaline phosphatase conjugates and chemiluminescence or chemifluorescence reagents.

Detection of a product comprising a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof, is indicative of the presence of BS200 mRNAs, suggesting a diagnosis of a breast tissue disease or condition, such as breast cancer.

#### Example 5: Northern Blotting

The Northern blot technique is used to identify a specific size RNA fragment from a complex population of RNA using gel electrophoresis and nucleic acid hybridization. Northern blotting is well-known technique in the art. Briefly, 5-10 µg of total RNA (see Example 3) are incubated in 15 µl of a solution containing 40 mM morpholinopropanesulfonic acid (MOPS) (pH 7.0), 10 mM sodium acetate, 1 mM EDTA, 2.2 M formaldehyde, 50% v/v formamide for 15 min at 65°C. The denatured RNA is mixed with 2 µl of loading buffer (50% glycerol, 1 mM EDTA, 0.4% bromophenol blue, 0.4% xylene cyanol) and loaded into a denaturing 1.0% agarose gel containing 40 mM MOPS (pH 7.0), 10 mM sodium acetate, 1 mM EDTA and 2.2 M formaldehyde. The gel is electrophoresed at 60 V for 1.5 hr and rinsed in RNase free water. RNA is transferred from the gel onto nylon membranes (Brightstar-Plus, Ambion, Inc., Austin, TX) for 1.5 hours using the downward alkaline capillary transfer method (Chomczynski, Anal. Biochem. 201:134-139, 1992). The filter is rinsed with 1X SSC, and RNA is crosslinked to the filter using a Stratalinker™ (Stratagene, Inc., La Jolla, CA) on the autocrosslinking mode and dried for 15 min. The membrane is then placed into a hybridization tube containing 20 ml of preheated prehybridization solution (5X SSC, 50% formamide, 5X Denhardt's solution, 100 µg/ml denatured salmon sperm DNA) and incubated in a 42°C hybridization oven for at least 3 hr. While the blot is prehybridizing, a <sup>32</sup>P-labeled random-primed probe is generated using the BS200 insert fragment (obtained by digesting clone 3021177 or another comparable clone with XbaI and NotI) using Random Primer DNA Labeling System (Life Technologies, Inc., Gaithersburg, MD) according to the manufacturer's instructions. Half of the probe is boiled for 10 min, quick chilled on ice and added to the hybridization tube. Hybridization is carried out at 42°C for at least 12 hr. The hybridization solution

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is discarded and the filter is washed in 30 ml of 3X SSC, 0.1% SDS at 42°C for 15 min, followed by 30 ml of 3X SSC, 0.1% SDS at 42°C for 15 min. The filter is wrapped in Saran Wrap, exposed to Kodak XAR-Omat film for 8-96 hr, and the film is developed for analysis. High level of expression of mRNA corresponding to a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof, is an indication of the presence of BS200 mRNA, suggesting a diagnosis of a breast tissue disease or condition, such as breast cancer.

#### Example 6: Dot Blot/Slot Blot

Dot and slot blot assays are quick methods to evaluate the presence of a specific nucleic acid sequence in a complex mix of nucleic acid. To perform such assays, up to 50 µg of RNA are mixed in 50 µl of 50% formamide, 7% formaldehyde, 1X SSC, incubated 15 min at 68°C, and then cooled on ice. Then, 100 µl of 20X SSC are added to the RNA mixture and loaded under vacuum onto a manifold apparatus that has a prepared nitrocellulose or nylon membrane. The membrane is soaked in water, 20X SSC for 1 hour, placed on two sheets of 20X SSC prewet Whatman #3 filter paper, and loaded into a slot blot or dot blot vacuum manifold apparatus. The slot blot is analyzed with probes prepared and labeled as described in Example 4, supra. Detection of mRNA corresponding to a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof, is an indication of the presence of BS200, suggesting a diagnosis of a breast tissue disease or condition, such as breast cancer.

Other methods and buffers which can be utilized in the methods described in Examples 5 and 6, but not specifically detailed herein, are known in the art and are described in J. Sambrook et al., supra.

#### Example 7: In Situ Hybridization

This method is useful to directly detect specific target nucleic acid sequences in cells using detectable nucleic acid hybridization probes.

Tissues are prepared with cross-linking fixative agents such as paraformaldehyde or glutaraldehyde for maximum cellular RNA retention. See, L. Angerer et al., Methods in Cell Biol. 35:37-71 (1991). Briefly, the tissue is placed in greater than 5 volumes of 1% glutaraldehyde in 50 mM sodium phosphate, pH 7.5 at 4°C for 30 min. The solution is changed with fresh

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glutaraldehyde solution (1% glutaraldehyde in 50 mM sodium phosphate, pH 7.5) for a further 30 min fixing. The fixing solution should have an osmolality of approximately 0.375% NaCl. The tissue is washed once in isotonic NaCl to remove the phosphate.

The fixed tissues then are embedded in paraffin as follows. The tissue is dehydrated through a series of increasing ethanol concentrations for 15 min each: 50% (twice), 70% (twice), 85%, 90% and then 100% (twice). Next, the tissue is soaked in two changes of xylene for 20 min each at room temperature. The tissue is then soaked in two changes of a 1:1 mixture of xylene and paraffin for 20 min each at 60°C; and then in three final changes of paraffin for 15 min each.

Next, the tissue is cut in 5  $\mu$ m sections using a standard microtome and placed on a slide previously treated with a tissue adhesive such as 3-aminopropyltriethoxysilane.

Paraffin is removed from the tissue by two 10 min xylene soaks and rehydrated in a series of decreasing ethanol concentrations: 99% (twice), 95%, 85%, 70%, 50%, and 30%; and then in distilled water (twice). The sections are pre-treated with 0.2 M HCl for 10 min and permeabilized with 2  $\mu$ g/ml Proteinase K at 37°C for 15 min.

Labeled riboprobes transcribed from the BS200 gene plasmid (see Example 4) are hybridized to the prepared tissue sections and incubated overnight at 56°C in 3X standard saline extract and 50% formamide. Excess probe is removed by washing in 2X standard saline citrate and 50% formamide followed by digestion with 100  $\mu$ g/ml RNase A at 37°C for 30 min. Fluorescence probe is visualized by illumination with ultraviolet (UV) light under a microscope. Fluorescence in the cytoplasm is indicative of BS200 mRNA. Alternatively, the sections can be visualized by autoradiography.

#### Example 8: Reverse Transcription PCR

A. One Step RT-PCR Assay. Target-specific primers are designed to detect the above-described target sequences by reverse transcription PCR using methods known in the art. One step RT-PCR is a sequential procedure that performs both RT and PCR in a single reaction mixture. The procedure is performed in a 200  $\mu$ l reaction mixture containing 50 mM (N,N,-bis[2-Hydroxyethyl]glycine), pH 8.15, 81.7 mM KOAc, 33.33 mM KOH, 0.01 mg/ml bovine serum albumin, 0.1 mM ethylene diaminetetraacetic acid, 0.02 mg/ml  $\text{NaN}_3$ , 8% w/v glycerol, 150  $\mu$ M each of dNTP, 0.25  $\mu$ M each primer, 5U rTth

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polymerase, 3.25 mM Mn(OAc)<sub>2</sub> and 5 µl of target RNA (see Example 3). Since RNA and the rTth polymerase enzyme are unstable in the presence of Mn(OAc)<sub>2</sub>, the Mn(OAc)<sub>2</sub> should be added just before target addition. Optimal conditions for cDNA synthesis and thermal cycling readily can be determined by those skilled in the art. The reaction is incubated in a Perkin-Elmer Thermal Cycler 480. Conditions which may be found useful include cDNA synthesis at 60°-70°C for 15-45 min and 30-45 amplification cycles at 94°C, 1 min; 55°-70°C, 1 min; 72°C, 2 min. One step RT-PCR also may be performed by using a dual enzyme procedure with Taq polymerase and a reverse transcriptase enzyme, such as MMLV (Moloney murine leukemia virus) or AMV (avian myeloblastosis virus) RT (reverse transcriptase) enzymes.

B. Traditional RT-PCR. A traditional two-step RT-PCR reaction was performed, as described by K.Q. Hu et al., *Virology* 181:721-726 (1991). Briefly, 0.5 µg of extracted RNA (see Example 3) was reverse transcribed in a 20 µl reaction mixture containing 1X PCR II buffer (Perkin-Elmer), 5 mM MgCl<sub>2</sub>, 1 mM dNTP, 20 U RNasin, 2.5 µM random hexamers, and 50 U MMLV (Moloney murine leukemia virus) reverse transcriptase (RT). Reverse transcription was performed at room temperature for 10 min, 42°C for 60 min in a PE-480 thermal cycler, followed by further incubation at 95°C for 5 min to inactivate the RT. PCR was performed using 2 µl of the cDNA reaction in a final PCR reaction volume of 50 µl containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 2 mM MgCl<sub>2</sub>, 200 µM dNTP, 0.5 µM of each sense and antisense primer (SEQUENCE ID NO 29 and SEQUENCE ID NO 30, respectively), and 2.5 U of Taq polymerase. The reaction was incubated in an MJ Research Model PTC-200 as follows: 35 cycles of amplification (94°C, 45 sec; 65°C, 45 sec; 72°C, 2 min); a final extension (72°C, 7 min); and a soak at 4°C.

C. PCR Fragment Analysis. The correct products were verified by size determination using gel electrophoresis with ethidium bromide staining (0.5 µg/ml) and visualized by UV illumination (Figures 3A and 3B). Figure 3A shows PCR generated DNA bands of approximately 332 bp, as indicated by DNA size markers (Lane 6), which are indicative of a BS200-specific PCR product in normal breast tissue (lanes 1-5), breast cancer tissue (lanes 8, 9, and 11), and the MCF7 cell line (lane 11) but not from placental DNA (lane 14). Figure 3B shows that the BS200-specific band at 332 bp was not observed in the five normal lung and lung cancer tissues tested (lanes 1-5), nor in the five normal colon and colon cancer tissues tested (lanes 7-11). Detection of a product

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comprising a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof, indicates the presence of BS200 mRNA in breast tissue, suggesting a diagnosis of a breast tissue disease or condition, such as breast cancer.

#### Example 9: OH-PCR

A. Probe selection and Labeling. Target-specific primers and probes are designed to detect the above-described target sequences by oligonucleotide hybridization PCR. International Publication Nos WO 92/10505, published June 25, 1992, and WO 92/11388, published July 9, 1992, teach methods for labeling oligonucleotides at their 5' and 3' ends, respectively. According to one known method for labeling an oligonucleotide, a label-phosphoramidite reagent is prepared and used to add the label to the oligonucleotide during its synthesis. For example, see N. T. Thuong et al., Tet. Letters 29(46):5905-5908 (1988); or J. S. Cohen et al., published U.S. Patent Application 07/246,688 (NTIS ORDER No. PAT-APPL-7-246,688) (1989). Preferably, probes are labeled at their 3' end to prevent participation in PCR and the formation of undesired extension products. For one step OH-PCR, the probe should have a  $T_M$  at least 15°C below the  $T_M$  of the primers. The primers and probes are utilized as specific binding members, with or without detectable labels, using standard phosphoramidite chemistry and/or post-synthetic labeling methods which are well-known to one skilled in the art.

B. One Step Oligo Hybridization PCR. OH-PCR is performed on a 200  $\mu$ l reaction containing 50 mM (N,N-bis[2-Hydroxyethyl]glycine), pH 8.15, 81.7 mM KOAc, 33.33 mM KOH, 0.01 mg/ml bovine serum albumin, 0.1 mM ethylene diaminetetraacetic acid, 0.02 mg/ml  $\text{NaN}_3$ , 8% w/v glycerol, 150  $\mu$ M each of dNTP, 0.25  $\mu$ M each primer, 3.75 nM probe, 5U rTth polymerase, 3.25 mM  $\text{Mn}(\text{OAc})_2$  and 5  $\mu$ l blood equivalents of target (see Example 3). Since RNA and the rTth polymerase enzyme are unstable in the presence of  $\text{Mn}(\text{OAc})_2$ , the  $\text{Mn}(\text{OAc})_2$  should be added just before target addition. The reaction is incubated in a Perkin-Elmer Thermal Cycler 480. Optimal conditions for cDNA synthesis and thermal cycling can be readily determined by those skilled in the art. Conditions which may be found useful include cDNA synthesis (60°C, 30 min), 30-45 amplification cycles (94°C, 40 sec; 55-70°C, 60 sec), oligo-hybridization (97°C, 5 min; 15°C, 5 min; 15°C soak). The correct

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reaction product contains at least one of the strands of the PCR product and an internally hybridized probe.

C. OH-PCR Product Analysis. Amplified reaction products are detected on an LCx<sup>®</sup> Analyzer system (available from Abbott Laboratories, Abbott Park, IL). Briefly, the correct reaction product is captured by an antibody labeled microparticle at a capturable site on either the PCR product strand or the hybridization probe, and the complex is detected by binding of a detectable antibody conjugate to either a detectable site on the probe or the PCR strand. Only a complex containing a PCR strand hybridized with the internal probe is detectable. The detection of this complex then is indicative of the presence of BS200 mRNA, suggesting a diagnosis of a breast disease or condition, such as breast cancer.

Many other detection formats exist which can be used and/or modified by those skilled in the art to detect the presence of amplified or non-amplified BS200-derived nucleic acid sequences including, but not limited to, ligase chain reaction (LCR, Abbott Laboratories, Abbott Park, IL); Q-beta replicase (Gene-Trak<sup>™</sup>, Naperville, Illinois), branched chain reaction (Chiron, Emeryville, CA) and strand displacement assays (Becton Dickinson, Research Triangle Park, NC).

#### Example 10: Synthetic Peptide Production

Synthetic peptides were modeled and then prepared based upon the predicted amino acid sequence of the BS200 polypeptide consensus sequence (see Example 1). In particular, a number of BS200 peptides derived from SEQUENCE ID NO 31 were prepared, including the peptides of SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, and SEQUENCE ID NO 35. All peptides were synthesized on a Symphony Peptide Synthesizer (available from Rainin Instrument Co, Emeryville, CA) or similar instrument, using Fmoc chemistry, standard cycles and in-situ HBTU activation. Cleavage and deprotection conditions were as follows: a volume of 2.5 ml of cleavage reagent (77.5% v/v trifluoroacetic acid, 15% v/v ethanedithiol, 2.5% v/v water, 5% v/v thioanisole, 1-2% w/v phenol) were added to the resin, and agitated at room temperature for 2-4 hours. The filtrate was then removed and the peptide was precipitated from the cleavage reagent with cold diethyl ether. Each peptide was filtered, purified via reverse-phase preparative HPLC using a



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water/acetonitrile/0.1% TFA gradient, and lyophilized. The product was confirmed by mass spectrometry.

The purified peptides were used to immunize animals (see Example 14).

Example 11a: Expression of Protein in a Cell Line Using Plasmid 577

A. Construction of a BS200 Expression Plasmid. Plasmid 577, described in U.S. patent application Serial No. 08/478,073, filed June 7, 1995, has been constructed for the expression of secreted antigens in a permanent cell line. This plasmid contains the following DNA segments: (a) a 2.3 kb fragment of pBR322 containing bacterial beta-lactamase and origin of DNA replication; (b) a 1.8 kb cassette directing expression of a neomycin resistance gene under control of HSV-1 thymidine kinase promoter and poly-A addition signals; (c) a 1.9 kb cassette directing expression of a dihydrofolate reductase gene under the control of an Simian Virus 40 (SV40) promoter and poly-A addition signals; (d) a 3.5 kb cassette directing expression of a rabbit immunoglobulin heavy chain signal sequence fused to a modified hepatitis C virus (HCV) E2 protein under the control of the Simian Virus 40 T-Ag promoter and transcription enhancer, the hepatitis B virus surface antigen (HBsAg) enhancer I followed by a fragment of Herpes Simplex Virus-1 (HSV-1) genome providing poly-A addition signals; and (e) a residual 0.7 kb fragment of SV40 genome late region of no function in this plasmid. All of the segments of the vector were assembled by standard methods known to those skilled in the art of molecular biology.

Plasmids for the expression of secretable BS200 proteins are constructed by replacing the hepatitis C virus E2 protein coding sequence in plasmid 577 with that of a BS200 polynucleotide sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof, as follows. Digestion of plasmid 577 with XbaI releases the hepatitis C virus E2 gene fragment. The resulting plasmid backbone allows insertion of the BS200 cDNA insert downstream of the rabbit immunoglobulin heavy chain signal sequence which directs the expressed proteins into the secretory pathway of the cell. The BS200 cDNA fragment is generated by PCR using standard procedures. Encoded in the sense PCR primer sequence is an XbaI site, immediately followed by a 12 nucleotide sequence that encodes the amino acid sequence Ser-Asn-Glu-Leu ("SNEL") to promote signal protease processing, efficient secretion and final product stability in culture fluids. Immediately following this 12 nucleotide sequence the primer contains nucleotides

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complementary to template sequences encoding amino acids of the BS200 gene. The antisense primer incorporates a sequence encoding the following eight amino acids just before the stop codons: Asp-Tyr-Lys-Asp-Asp-Asp-Asp-Lys (SEQUENCE ID NO 36). Within this sequence is incorporated a recognition site to aid in analysis and purification of the BS200 protein product. A recognition site (termed "FLAG") that is recognized by a commercially available monoclonal antibody designated anti-FLAG M2 (Eastman Kodak, Co., New Haven, CT) can be utilized, as well as other comparable sequences and their corresponding antibodies. For example, PCR is performed using GeneAmp<sup>®</sup> reagents obtained from Perkin-Elmer-Cetus, as directed by the supplier's instructions. PCR primers are used at a final concentration of 0.5  $\mu$ M. PCR is performed on the BS200 plasmid template in a 100  $\mu$ l reaction for 35 cycles (94°C, 30 seconds; 55°C, 30 seconds; 72°C, 90 seconds) followed by an extension cycle of 72°C for 10 min.

B. Transfection of Dihydrofolate Reductase Deficient Chinese Hamster Ovary Cells. The plasmid described supra is transfected into CHO/dhfr- cells [DXB-111, Uriacio et al., PNAS 77:4451-4466 (1980)]. These cells are available from the A.T.C.C., 12301 Parklawn Drive, Rockville, MD 20852, under Accession No. CRL 9096. Transfection is carried out using the cationic liposome-mediated procedure described by P. L. Felgner et al., PNAS 84:7413-7417 (1987). Particularly, CHO/dhfr- cells are cultured in Ham's F-12 media supplemented with 10% fetal calf serum, L-glutamine (1 mM) and freshly seeded into a flask at a density of  $5-8 \times 10^5$  cells per flask. The cells are grown to a confluency of between 60 and 80% for transfection. Twenty micrograms (20 $\mu$ g) of plasmid DNA are added to 1.5 ml of Opti-MEM I medium and 100  $\mu$ l of Lipofectin Reagent (Gibco-BRL; Grand Island, NY) are added to a second 1.5 ml portion of Opti-MEM I media. The two solutions are mixed and incubated at room temperature for 20 min. After the culture medium is removed from the cells, the cells are rinsed 3 times with 5 ml of Opti-MEM I medium. The Opti-MEM I-Lipofection-plasmid DNA solution then is overlaid onto the cells. The cells are incubated for 3 hr at 37°C, after which time the Opti-MEM I-Lipofectin-DNA solution is replaced with culture medium for an additional 24 hr prior to selection.

C. Selection and Amplification. One day after transfection, cells are passaged 1:3 and incubated with dhfr/G418 selection medium (hereafter, "F-12 minus medium G"). Selection medium is Ham's F-12 with L-glutamine and

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without hypoxanthine, thymidine and glycine (JRH Biosciences, Lenexa, Kansas) and 300 µg per ml G418 (Gibco-BRL; Grand Island, NY). Media volume-to-surface area ratios of 5 ml per 25 cm<sup>2</sup> are maintained. After approximately two weeks, DHFR/G418 cells are expanded to allow passage and continuous maintenance in F-12 minus medium G.

Amplification of each of the transfected BS200 cDNA sequences is achieved by stepwise selection of DHFR<sup>+</sup>, G418<sup>+</sup> cells with methotrexate (reviewed by R. Schimke, Cell 37:705-713 [1984]). Cells are incubated with F-12 minus medium G containing 150 nM methotrexate (MTX) (Sigma, St. Louis, MO) for approximately two weeks until resistant colonies appear. Further gene amplification is achieved by selection of 150 nM adapted cells with 5 µM MTX.

D. Antigen Production. F-12 minus medium G supplemented with 5 µM MTX is overlaid onto just confluent monolayers for 12 to 24 hr at 37°C in 5% CO<sub>2</sub>. The growth medium is removed and the cells are rinsed 3 times with Dulbecco's phosphate buffered saline (PBS) (with calcium and magnesium) (Gibco-BRL; Grand Island, NY) to remove the remaining media/serum which may be present. Cells then are incubated with VAS custom medium (VAS custom formulation with L-glutamine with HEPES without phenol red, available from JRH Bioscience; Lenexa, KS, product number 52-08678P), for 1 hr at 37°C in 5% CO<sub>2</sub>. Cells then are overlaid with VAS for production at 5 ml per T flask. Medium is removed after seven days of incubation, retained, and then frozen to await purification with harvests 2, 3 and 4. The monolayers are overlaid with VAS for 3 more seven day harvests.

E. Analysis of Breast Tissue Gene BS200 Antigen Expression. Aliquots of VAS supernatants from the cells expressing the BS200 protein construct are analyzed, either by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) using standard methods and reagents known in the art (Laemmli discontinuous gels), or by mass spectrometry.

F. Purification. Purification of the BS200 protein containing the FLAG sequence is performed by immunoaffinity chromatography using an affinity matrix comprising anti-FLAG M2 monoclonal antibody covalently attached to agarose by hydrazide linkage (Eastman Kodak Co., New Haven, CT). Prior to affinity purification, protein in pooled VAS medium harvests from roller bottles is exchanged into 50 mM Tris-HCl (pH 7.5), 150 mM NaCl buffer using a Sephadex G-25 (Pharmacia Biotech Inc., Uppsala, Sweden) column. Protein in this buffer is applied to the anti-FLAG M2 antibody affinity column. Non-

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binding protein is eluted by washing the column with 50 mM Tris-HCl (pH 7.5), 150 mM NaCl buffer. Bound protein is eluted using an excess of FLAG peptide in 50 mM Tris-HCl (pH 7.5), 150 mM NaCl. The excess FLAG peptide can be removed from the purified BS200 protein by gel electrophoresis or HPLC.

Although plasmid 577 is utilized in this example, it is known to those skilled in the art that other comparable expression systems, such as CMV, can be utilized herein with appropriate modifications in reagent and/or techniques and are within the skill of the ordinary artisan.

The largest cloned insert containing the coding region of the BS200 gene is then sub-cloned into either (i) a eukaryotic expression vector which may contain, for example, a cytomegalovirus (CMV) promoter and/or protein fusible sequences which aid in protein expression and detection, or (ii) a bacterial expression vector containing a superoxide-dismutase (SOD) and CMP-KDO synthetase (CKS) or other protein fusion gene for expression of the protein sequence. Methods and vectors which are useful for the production of polypeptides which contain fusion sequences of SOD are described in EPO 0196056, published October 1, 1986, and those containing fusion sequences of CKS are described in EPO Publication No. 0331961, published September 13, 1989. This so-purified protein can be used in a variety of techniques, including, but not limited to animal immunization studies, solid phase immunoassays, etc.

Example 11b: Expression of Protein in a Cell Line Using pcDNA3.1/Myc-His

A. Construction of a BS200 Expression Plasmid. Plasmid pcDNA3.1/Myc-His (Cat.# V855-20, Invitrogen, Carlsbad, CA) has been constructed, in the past, for the expression of secreted antigens by most mammalian cell lines. Expressed protein inserts are fused to a myc-his peptide tag. The myc-his tag is a 21 residue amino acid sequence having the following sequence: Glu-Gln-Lys-Leu-Ile-Ser-Glu- Glu-Asp-Leu-Asn-Met-His-Thr-Glu-His-His-His-His-His-His (SEQUENCE ID NO 37) and comprises a c-myc oncoprotein epitope and a polyhistidine sequence which are useful for the purification of an expressed fusion protein by using either anti-myc or anti-his affinity columns, or metalloprotein binding columns.

Plasmids for the expression of secretable BS200 proteins are constructed by inserting a BS200 polynucleotide sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof. Prior to

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construction of a BS200 expression plasmid, the BS200 cDNA sequence is first cloned into a pCR<sup>®</sup>-Blunt vector as follows:

The BS200 cDNA fragment is generated by PCR using standard procedures. For example, PCR is performed procedures and reagents from Stratagene<sup>®</sup>, Inc. (La Jolla, CA), as directed by the manufacturer. PCR primers are used at a final concentration of 0.5  $\mu$ M. PCR using 5 U of pfu polymerase (Stratagene, La Jolla, CA) is performed on the BS200 plasmid template (see Example 2) in a 50  $\mu$ l reaction for 30 cycles (94°C, 1 min; 65°C, 1.5 min; 72°C, 3 min) followed by an extension cycle of 72°C for 8 min. (The sense PCR primer sequence comprises nucleotides which are either complementary to the pINCY vector directly upstream of the BS200 gene insert or which incorporate a 5' EcoRI restriction site, an adjacent downstream protein translation consensus initiator, and a 3' nucleic acid sequence which is the same sense as the 5'-most end of the BS200 cDNA insert. The antisense PCR primer incorporates a 5' NotI restriction sequence and a sequence complementary to the 3' end of the BS200 cDNA insert just upstream of the 3'-most, in-frame stop codon.) Five microliters (5  $\mu$ l) of the resulting blunted-ended PCR product are ligated into 25 ng of linearized pCR<sup>®</sup>-Blunt vector (Invitrogen, Carlsbad, CA) interrupting the lethal ccdB gene of the vector. The resulting ligated vector is transformed into TOP10 *E. coli* (Invitrogen, Carlsbad, CA) using a One Shot<sup>™</sup> Transformation Kit (Invitrogen, Carlsbad, CA) following manufacturer's instructions. The transformed cells are grown on LB-Kan (50  $\mu$ g/ml kanamycin) selection plates at 37°C. Only cells containing a plasmid with an interrupted ccdB gene will grow after transformation [Grant, S.G.N., *PNAS* 87:4645-4649 (1990)]. Transformed colonies are picked and grown up in 3 ml of LB-Kan broth at 37°C. Plasmid DNA is isolated by using a QIAprep<sup>®</sup> (Qiagen Inc., Santa Clarita, CA) procedure, as directed by the manufacturer. The DNA is cut with EcoRI or SnaBI, and NotI restriction enzymes to release the BS200 insert fragment. The fragment is run on 1% Seakem<sup>®</sup> LE agarose/0.5  $\mu$ g/ml ethidium bromide/TE gel, visualized by UV irradiation, excised and purified using QIAquick<sup>™</sup> (Qiagen Inc., Santa Clarita, CA) procedures, as directed by the supplier's instructions.

The pcDNA3.1/Myc-His plasmid DNA is linearized by digestion with EcoRI or SnaBI, and NotI in the polylinker region of the plasmid DNA. The resulting plasmid DNA backbone allows insertion of the BS200 purified cDNA fragment, supra, downstream of a CMV promoter which directs expression of the proteins in mammalian cells. The ligated plasmid is transformed into DH5

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alpha<sup>TM</sup> cells (GibcoBRL Grand Island, NY), as directed by the manufacturer. Briefly, 10 ng of pcDNA3.1/Myc-His containing a BS200 insert are added to 50 µl of competent DH5 alpha cells, and the contents are mixed gently. The mixture is incubated on ice for 30 min, heat shocked for 20 sec at 37°C, and placed on ice for an additional 2 min. Upon addition of 0.95 ml of LB medium, the mixture is incubated for 1 hr at 37°C while shaking at 225 rpm. The transformed cells then are plated onto 100 mm LB/Amp (50µg/ml ampicillin) plates and grown at 37°C. Colonies are picked and grown in 3 ml of LB/Amp broth. Plasmid DNA is purified using a QIAprep kit. The presence of the insert is confirmed using techniques known to those skilled in the art, including, but not limited to restriction digestion and gel analysis. (J. Sambrook et al., supra.)

B. Transfection of Human Embryonic Kidney Cell 293 Cells. The BS200 expression plasmid described in section A, supra, is retransformed into DH5 alpha cells, plated onto LB/ampicillin agar, and grown up in 10 ml of LB/ampicillin broth, as described hereinabove. The plasmid is purified using a QIAfilter<sup>TM</sup> Maxi Kit (Qiagen, Chatsworth, CA) and is transfected into HEK293 cells [F.L. Graham et al., J. Gen. Vir. 36:59-72 (1977)]. These cells are available from the A.T.C.C., 12301 Parklawn Drive, Rockville, MD 20852, under Accession No. CRL 1573. Transfection is carried out using the cationic lipofectamine-mediated procedure described by P. Hawley-Nelson et al., Focus 15:73 (1993). Particularly, HEK293 cells are cultured in 10 ml DMEM media supplemented with 10% fetal bovine serum (FBS), L-glutamine (2 mM) and freshly seeded into 100 mm culture plates at a density of  $9 \times 10^6$  cells per plate. The cells are grown at 37 °C to a confluency of between 70% and 80% for transfection. Eight micrograms (8 µg) of plasmid DNA are added to 800 µl of Opti-MEM I<sup>®</sup> medium (Gibco-BRL, Grand Island, NY), and 48-96 µl of Lipofectamine<sup>TM</sup> Reagent (Gibco-BRL, Grand Island, NY) are added to a second 800 µl portion of Opti-MEM I media. The two solutions are mixed and incubated at room temperature for 15-30 min. After the culture medium is removed from the cells, the cells are washed once with 10 ml of serum-free DMEM. The Opti-MEM I-Lipofectamine-plasmid DNA solution is diluted with 6.4 ml of serum-free DMEM and then overlaid onto the cells. The cells are incubated for 5 hr at 37°C, after which time, an additional 8 ml of DMEM with 20% FBS are added. After 18-24 hr, the old medium is aspirated, and the cells are overlaid with 5 ml of fresh DMEM with 5% FBS. Supernatants and cell extracts are analyzed for BS200 gene activity 72 hr after transfection.

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C. Analysis of Breast Tissue Gene BS200 Antigen Expression. The culture supernatant, supra, is transferred to cryotubes and stored on ice. HEK293 cells are harvested by washing twice with 10 ml of cold Dulbecco's PBS and lysing by addition of 1.5 ml of CAT lysis buffer (Boehringer Mannheim, Indianapolis, IN), followed by incubation for 30 min at room temperature. Lysate is transferred to 1.7 ml polypropylene microfuge tubes and centrifuged at 1000 x g for 10 min. The supernatant is transferred to new cryotubes and stored on ice. Aliquots of supernatants from the cells and the lysate of the cells expressing the BS200 protein construct are analyzed for the presence of BS200 recombinant protein. The aliquots can be run on SDS-polyacrylamide gel electrophoresis (SDS-PAGE) using standard methods and reagents known in the art. (J. Sambrook et al., supra) These gels can then be blotted onto a solid medium such as nitrocellulose, nytran, etc., and the BS200 protein band can be visualized using Western blotting techniques with anti-myc epitope or anti-histidine monoclonal antibodies (Invitrogen, Carlsbad, CA) or anti-BS200 polyclonal serum (see Example 14). Alternatively, the expressed BS200 recombinant protein can be analyzed by mass spectrometry (see Example 12).

D. Purification. Purification of the BS200 recombinant protein containing the myc-his sequence is performed using the Xpress<sup>®</sup> affinity chromatography system (Invitrogen, Carlsbad, CA) containing a nickel-charged agarose resin which specifically binds polyhistidine residues. Supernatants from 10 x 100 mm plates, prepared as described supra, are pooled and passed over the nickel-charged column. Non-binding protein is eluted by washing the column with 50 mM Tris-HCl (pH 7.5)/150 mM NaCl buffer, leaving only the myc-his fusion proteins. Bound BS200 recombinant protein then is eluted from the column using either an excess of imidazole or histidine, or a low pH buffer. Alternatively, the recombinant protein can also be purified by binding at the myc-his sequence to an affinity column consisting of either anti-myc or anti-histidine monoclonal antibodies conjugated through a hydrazide or other linkage to an agarose resin and eluting with an excess of myc peptide or histidine, respectively.

The purified recombinant protein can then be covalently cross-linked to a solid phase, such as N-hydroxysuccinimide-activated sepharose columns (Pharmacia Biotech, Piscataway, NJ), as directed by supplier's instructions. These columns containing covalently linked BS200 recombinant protein, can

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then be used to purify anti-BS200 antibodies from rabbit or mouse sera (see Examples 13 and 14).

E. Coating Microtiter Plates with BS200 Expressed Proteins.

Supernatant from a 100 mm plate, as described *supra*, is diluted in an appropriate volume of PBS. Then, 100  $\mu$ l of the resulting mixture is placed into each well of a Reacti-Bind<sup>TM</sup> metal chelate microtiter plate (Pierce, Rockford, IL), incubated at room temperature while shaking, and followed by three washes with 200  $\mu$ l each of PBS with 0.05% Tween<sup>®</sup> 20. The prepared microtiter plate can then be used to screen polyclonal antisera for the presence of BS200 antibodies (see Example 17).

Although pcDNA3.1/Myc-His is utilized in this example, it is known to those skilled in the art that other comparable expression systems can be utilized herein with appropriate modifications in reagent and/or techniques and are within the skill of one of ordinary skill in the art. The largest cloned insert containing the coding region of the BS200 gene is sub-cloned into either (i) a eukaryotic expression vector which may contain, for example, a cytomegalovirus (CMV) promoter and/or protein fusible sequences which aid in protein expression and detection, or (ii) a bacterial expression vector containing a superoxide-dismutase (SOD) and CMP-KDO synthetase (CKS) or other protein fusion gene for expression of the protein sequence. Methods and vectors which are useful for the production of polypeptides which contain fusion sequences of SOD are described in published EPO application No. EP 0 196 056, published October 1, 1986, and vectors containing fusion sequences of CKS are described in published EPO application No. EP 0 331 961, published September 13, 1989. The purified protein can be used in a variety of techniques, including, but not limited to animal immunization studies, solid phase immunoassays, etc.

Example 12: Chemical Analysis of Breast Tissue Proteins

A. Analysis of Tryptic Peptide Fragments Using MS. Sera from patients with breast disease, such as breast cancer, sera from patients with no breast disease, extracts of breast tissues or cells from patients with breast disease, such as breast cancer, extracts of breast tissues or cells from patients with no breast disease, and extracts of tissues or cells from other non-diseased or diseased organs of patients, are run on a polyacrylamide gel using standard procedures and stained with Coomassie Blue. Sections of the gel suspected of containing the unknown polypeptide are excised and subjected to an in-gel reduction,



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acetamidation and tryptic digestion. P. Jenö et al., Anal. Bio. 224:451-455 (1995) and J. Rosenfeld et al., Anal. Bio. 203:173-179 (1992). The gel sections are washed with 100 mM  $\text{NH}_4\text{HCO}_3$  and acetonitrile. The shrunken gel pieces are swollen in digestion buffer (50 mM  $\text{NH}_4\text{HCO}_3$ , 5 mM  $\text{CaCl}_2$  and 12.5  $\mu\text{g/ml}$  trypsin) at 4°C for 45 min. The supernatant is aspirated and replaced with 5 to 10  $\mu\text{l}$  of digestion buffer without trypsin and allowed to incubate overnight at 37°C. Peptides are extracted with 3 changes of 5% formic acid and acetonitrile and evaporated to dryness. The peptides are adsorbed to approximately 0.1  $\mu\text{l}$  of POROS R2 sorbent (Perseptive Biosystems, Framingham, Massachusetts) trapped in the tip of a drawn gas chromatography capillary tube by dissolving them in 10  $\mu\text{l}$  of 5% formic acid and passing it through the capillary. The adsorbed peptides are washed with water and eluted with 5% formic acid in 60% methanol. The eluant is passed directly into the spraying capillary of an API III mass spectrometer (Perkin-Elmer Sciex, Thornhill, Ontario, Canada) for analysis by nano-electrospray mass spectrometry. M. Wilm et al., Int. J. Mass Spectrom. Ion Process 136:167-180 (1994) and M. Wilm et al., Anal. Chem. 66:1-8 (1994). The masses of the tryptic peptides are determined from the mass spectrum obtained off the first quadrupole. Masses corresponding to predicted peptides can be further analyzed in MS/MS mode to give the amino acid sequence of the peptide.

**B. Peptide Fragment Analysis Using LC/MS.** The presence of polypeptides predicted from mRNA sequences found in hyperplastic disease tissues also can be confirmed using liquid chromatography/tandem mass spectrometry (LC/MS/MS). D. Hess et al., METHODS, A Companion to Methods in Enzymology 6:227-238 (1994). The serum specimen or tumor extract from the patient is denatured with SDS and reduced with dithiothreitol (1.5 mg/ml) for 30 min at 90°C followed by alkylation with iodoacetamide (4 mg/ml) for 15 min at 25°C. Following acrylamide electrophoresis, the polypeptides are electroblotted to a cationic membrane and stained with Coomassie Blue. Following staining, the membranes are washed and sections thought to contain the unknown polypeptides are cut out and dissected into small pieces. The membranes are placed in 500  $\mu\text{l}$  microcentrifuge tubes and immersed in 10 to 20  $\mu\text{l}$  of proteolytic digestion buffer (100 mM Tris-HCl, pH 8.2, containing 0.1 M NaCl, 10% acetonitrile, 2 mM  $\text{CaCl}_2$  and 5  $\mu\text{g/ml}$  trypsin) (Sigma, St. Louis, MO). After 15 hr at 37°C, 3  $\mu\text{l}$  of saturated urea and 1  $\mu\text{l}$  of 100  $\mu\text{g/ml}$  trypsin are added and incubated for an additional 5 hr at 37°C. The

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digestion mixture is acidified with 3  $\mu$ l of 10% trifluoroacetic acid and centrifuged to separate supernatant from membrane. The supernatant is injected directly onto a microbore, reverse phase HPLC column and eluted with a linear gradient of acetonitrile in 0.05% trifluoroacetic acid. The eluate is fed directly into an electrospray mass spectrometer, after passing through a stream splitter if necessary to adjust the volume of material. The data is analyzed following the procedures set forth in Example 12, Section A.

#### Example 13: Gene Immunization Protocol

A. In Vivo Antigen Expression. Gene immunization circumvents protein purification steps by directly expressing an antigen *in vivo* after inoculation of the appropriate expression vector. Also, production of antigen by this method may allow correct protein folding and glycosylation since the protein is produced in mammalian tissue. The method utilizes insertion of the gene sequence into a plasmid which contains a CMV promoter, expansion and purification of the plasmid and injection of the plasmid DNA into the muscle tissue of an animal. Preferred animals include mice and rabbits. See, for example, H. Davis et al., Human Molecular Genetics 2:1847-1851 (1993). After one or two booster immunizations, the animal can then be bled, ascites fluid collected, or the animal's spleen can be harvested for production of hybridomas.

B. Plasmid Preparation and Purification. BS200 cDNA sequences are generated from the BS200 cDNA-containing vector using appropriate PCR primers containing suitable 5' restriction sites following the procedures described in Example 11. The PCR product is cut with appropriate restriction enzymes and inserted into a vector which contains the CMV promoter (for example, pRc/CMV or pcDNA3 vectors from Invitrogen, San Diego, CA). This plasmid then is expanded in the appropriate bacterial strain and purified from the cell lysate using a CsCl gradient or a Qiagen plasmid DNA purification column. All these techniques are familiar to one of ordinary skill in the art of molecular biology.

C. Immunization Protocol. Anesthetized animals are immunized intramuscularly with 0.1-100  $\mu$ g of the purified plasmid diluted in PBS or other DNA uptake enhancers (Cardiotoxin, 25% sucrose). See, for example, H. Davis et al., Human Gene Therapy 4:733-740 (1993); and P. W. Wolff et al., Biotechniques 11:474-485 (1991). One to two booster injections are given at monthly intervals.

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D. Testing and Use of Antiserum. Animals are bled and the resultant sera tested for antibody using peptides synthesized from the known gene sequence (see Example 16) using techniques known in the art, such as Western blotting or EIA techniques. Antisera produced by this method can then be used to detect the presence of the antigen in a patient's tissue or cell extract or in a patient's serum by ELISA or Western blotting techniques, such as those described in Examples 15 through 18.

Example 14: Production of Antibodies Against BS200

A. Production of Polyclonal Antisera. Antiserum against BS200 was prepared by injecting rabbits with peptides whose sequences were derived from that of the predicted amino acid sequence of the BS200 consensus nucleotide sequence (SEQUENCE ID NO 16). Synthesis of the BS200 peptides of SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, and SEQUENCE ID NO 35 is described in Example 10. Peptides used as immunogens were not conjugated to a carrier such as keyhole limpet hemocyanine, KLH, (i.e., they were unconjugated.).

Animal Immunization. Female white New Zealand rabbits weighing 2 kg or more were used for raising polyclonal antiserum. One animal was immunized per unconjugated BS200 peptide (SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, and SEQUENCE ID NO 35). One week prior to the first immunization, a 5 to 10 ml blood sample was obtained from each animal to serve as a non-immune prebleed sample.

Unconjugated BS200 peptides (SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, and SEQUENCE ID NO 35) were used to prepare the primary immunogen by emulsifying 0.5 ml of the peptide at a concentration of 2 mg/ml in PBS (pH 7.2) which contained 0.5 ml of complete Freund's adjuvant (CFA) (Difco, Detroit, MI). The immunogen was injected into several sites of the animal via subcutaneous, intraperitoneal, and intramuscular routes of administration. Four weeks following the primary immunization, a booster immunization was administered. The immunogen used for the booster immunization dose was prepared by emulsifying 0.5 ml of the same unconjugated peptide used for the primary immunogen, except that the peptide now was diluted to 1 mg/ml with 0.5 ml of incomplete Freund's adjuvant (IFA) (Difco, Detroit, MI). Again, the booster dose was administered into several sites via subcutaneous, intraperitoneal and intramuscular types of

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injections. The animals were bled (5 ml) two weeks after the booster immunizations and each serum was tested for immunoreactivity to the peptide as described below. The booster and bleed schedule was repeated at 4 week intervals until an adequate titer was obtained. The titer or concentration of antiserum was determined using unconjugated peptides in a microtiter EIA as described in Example 17, below. An antibody titer of 1:500 or greater was considered an adequate titer for further use and study.

Table 1. Titer of rabbit anti-BS200 peptide antisera (12 week bleed)

	<u>Peptide Immunogen</u>	<u>Titer</u>
SEQUENCE ID NO 32	2500	
SEQUENCE ID NO 33	>62,500	
SEQUENCE ID NO 34	>62,500	
SEQUENCE ID NO 35	61,000	

#### B. Production of Monoclonal Antibody.

1. Immunization Protocol. Mice are immunized using peptides which can either be conjugated to a carrier such as KLH [prepared as described hereinbelow, or unconjugated (i.e., not conjugated to a carrier such as KLH)] except that the amount of the unconjugated or conjugated peptide for monoclonal antibody production in mice is one-tenth the amount used to produce polyclonal antisera in rabbits. Thus, the primary immunogen consists of 100 µg of unconjugated or conjugated peptide in 0.1 ml of CFA emulsion while the immunogen used for booster immunizations consists of 50 µg of unconjugated or conjugated peptide in 0.1 ml of IFA. Hybridomas for the generation of monoclonal antibodies are prepared and screened using standard techniques. The methods used for monoclonal antibody development follow procedures known in the art such as those detailed in Kohler and Milstein, Nature 256:494 (1975) and reviewed in J.G.R. Hurrel, ed., Monoclonal Hybridoma Antibodies: Techniques and Applications, CRC Press, Inc., Boca Raton, FL (1982). Another method of monoclonal antibody development which is based on the Kohler and Milstein method is that of L.T. Mimms et al., Virology 176:604-619 (1990).

The immunization regimen (per mouse) consists of a primary immunization with additional booster immunizations. The primary immunogen

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used for the primary immunization consists of 100 µg of unconjugated or conjugated peptide in 50 µl of PBS (pH 7.2) previously emulsified in 50 µl of CFA. Booster immunizations performed at approximately two weeks and four weeks post primary immunization consist of 50 µg of unconjugated or conjugated peptide in 50 µl of PBS (pH 7.2) emulsified with 50 µl IFA. A total of 100 µl of this immunogen are inoculated intraperitoneally and subcutaneously into each mouse. Individual mice are screened for immune response by microtiter plate enzyme immunoassay (EIA) as described in Example 17 approximately four weeks after the third immunization. Mice are inoculated either intravenously, intrasplenically or intraperitoneally with 50 µg of unconjugated or conjugated peptide in PBS (pH 7.2) approximately fifteen weeks after the third immunization..

Three days after this intravenous boost, splenocytes are fused with, for example, Sp2/0-Ag14 myeloma cells (Milstein Laboratories, England) using the polyethylene glycol (PEG) method. The fusions are cultured in Iscove's Modified Dulbecco's Medium (IMDM) containing 10% fetal calf serum (FCS), plus 1% hypoxanthine, aminopterin and thymidine (HAT). Bulk cultures were screened by microtiter plate EIA following the protocol in Example 17. Clones reactive with the peptide used as an immunogen and non-reactive with other peptides (i.e., peptides of BS200 not used as the immunogen) are selected for final expansion. Clones thus selected are expanded, aliquoted and frozen in IMDM containing 10% FCS and 10% dimethyl sulfoxide, (DMSO).

2. Peptide Conjugation. Peptide is conjugated to maleimide activated KLH (commercially available as Imject<sup>®</sup>, available from Pierce Chemical Company, Rockford, IL). Imject<sup>®</sup> contains about 250 moles of reactive maleimide groups per mole of hemocyanine. The activated KLH is dissolved in phosphate buffered saline (PBS, pH 8.4) at a concentration of about 7.7 mg/ml. The peptide is conjugated through cysteines occurring in the peptide sequence, or to a cysteine previously added to the synthesized peptide in order to provide a point of attachment. The peptide is dissolved in DMSO (Sigma Chemical Company, St. Louis, MO) and reacted with the activated KLH at a mole ratio of about 1.5 moles of peptide per mole of reactive maleimide attached to the KLH. A procedure for the conjugation of peptide is provided hereinbelow. It is known to the ordinary artisan that the amounts, times and conditions of such a procedure can be varied to optimize peptide conjugation.

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The conjugation reaction described hereinbelow is based on obtaining 3 mg of KLH peptide conjugate ("conjugated peptide"), which contains about 0.77  $\mu$ moles of reactive maleimide groups. This quantity of peptide conjugate usually is adequate for one primary injection and four booster injections for production of polyclonal antisera in a rabbit. Briefly, peptide is dissolved in DMSO at a concentration of 1.16  $\mu$ moles/100  $\mu$ l of DMSO. One hundred microliters (100  $\mu$ l) of the DMSO solution are added to 380  $\mu$ l of the activated KLH solution prepared as described hereinabove, and 20  $\mu$ l of PBS (pH 8.4) are added to bring the volume to 500  $\mu$ l. The reaction is incubated overnight at room temperature with stirring. The extent of reaction is determined by measuring the amount of unreacted thiol in the reaction mixture. The difference between the starting concentration of thiol and the final concentration is assumed to be the concentration of peptide which has coupled to the activated KLH. The amount of remaining thiol is measured using Ellman's reagent (5,5'-dithiobis(2-nitrobenzoic acid), Pierce Chemical Company, Rockford, IL). Cysteine standards are made at a concentration of 0, 0.1, 0.5, 2, 5 and 20 mM by dissolving 35 mg of cysteine HCl (Pierce Chemical Company, Rockford, IL) in 10 ml of PBS (pH 7.2) and diluting the stock solution to the desired concentration(s). The photometric determination of the concentration of thiol is accomplished by placing 200  $\mu$ l of PBS (pH 8.4) in each well of an Immulon 2<sup>®</sup> microwell plate (Dynex Technologies, Chantilly, VA). Next, 10  $\mu$ l of standard or reaction mixture are added to each well. Finally, 20  $\mu$ l of Ellman's reagent at a concentration of 1 mg/ml in PBS (pH 8.4) are added to each well. The wells are incubated for 10 minutes at room temperature, and the absorbance of all wells is read at 415 nm with a microplate reader (such as the BioRad Model 3550, BioRad, Richmond, CA). The absorbance of the standards is used to construct a standard curve and the thiol concentration of the reaction mixture is determined from the standard curve. A decrease in the concentration of free thiol is indicative of a successful conjugation reaction. Unreacted peptide is removed by dialysis against PBS (pH 7.2) at room temperature for 6 hours. The conjugate is stored at 2-8°C if it is to be used immediately; otherwise, it is stored at -20°C or colder.

3. Production of Ascites Fluid Containing Monoclonal Antibodies. Frozen hybridoma cells prepared as described hereinabove are thawed and placed into expansion culture. Viable hybridoma cells are inoculated intraperitoneally into Pristane treated mice. Ascitic fluid is removed

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from the mice, pooled, filtered through a 0.2  $\mu$  filter and subjected to an immunoglobulin class G (IgG) analysis to determine the volume of the Protein A column required for the purification.

4. Purification of Monoclonal Antibodies From Ascites Fluid.

Briefly, filtered and thawed ascites fluid is mixed with an equal volume of Protein A sepharose binding buffer (1.5 M glycine, 3.0 M NaCl, pH 8.9) and refiltered through a 0.2  $\mu$  filter. The volume of the Protein A column is determined by the quantity of IgG present in the ascites fluid. The eluate then is dialyzed against PBS (pH 7.2) overnight at 2-8°C. The dialyzed monoclonal antibody is sterile filtered and dispensed in aliquots. The immunoreactivity of the purified monoclonal antibody is confirmed by determining its ability to specifically bind to the peptide used as the immunogen by use of the EIA microtiter plate assay procedure of Example 17. The specificity of the purified monoclonal antibody is confirmed by determining its lack of binding to irrelevant peptides such as peptides of BS200 not used as the immunogen. The purified anti-BS200 monoclonal thus prepared and characterized is placed at either 2-8°C for short term storage or at -80°C for long term storage.

5. Further Characterization of Monoclonal Antibody. The isotype and subtype of the monoclonal antibody produced as described hereinabove can be determined using commercially available kits (available from Amersham, Inc., Arlington Heights, IL). Stability testing also can be performed on the monoclonal antibody by placing an aliquot of the monoclonal antibody in continuous storage at 2-8°C and assaying optical density (OD) readings throughout the course of a given period of time.

C. Use of Recombinant Proteins as Immunogens. It is within the scope of the present invention that recombinant proteins made as described herein can be utilized as immunogens in the production of polyclonal and monoclonal antibodies, with corresponding changes in reagents and techniques known to those skilled in the art.

Example 15: Purification of Serum Antibodies Which Specifically Bind to BS200 Peptides

Immune sera, obtained as described hereinabove in Examples 13 and/or 14, is affinity purified using immobilized synthetic BS200 peptides prepared as described in Example 10, or recombinant BS200 proteins prepared as described in Example 11. An IgG fraction of the antiserum is obtained by passing the

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diluted, crude antiserum over a Protein A column (Affi-Gel protein A, Bio-Rad, Hercules, CA). Elution with a buffer (Binding Buffer, supplied by the manufacturer) removes substantially all proteins that are not immunoglobulins. Elution with 0.1 M buffered glycine (pH 3) gives an immunoglobulin preparation that is substantially free of albumin and other serum proteins.

Immunoaffinity chromatography is performed to obtain a preparation with a higher fraction of specific antigen-binding antibody. The peptide used to raise the antiserum is immobilized on a chromatography resin, and the specific antibodies directed against its epitopes are adsorbed to the resin. After washing away non-binding components, the specific antibodies are eluted with 0.1 M glycine buffer, pH 2.3. Antibody fractions are immediately neutralized with 1.0 M Tris buffer (pH 8.0) to preserve immunoreactivity. The chromatography resin chosen depends on the reactive groups present in the peptide. If the peptide has an amino group, a resin such as Affi-Gel 10 or Affi-Gel 15 is used (Bio-Rad, Hercules, CA). If coupling through a carboxy group on the peptide is desired, Affi-Gel 102 can be used (Bio-Rad, Hercules, CA). If the peptide has a free sulfhydryl group, an organomercurial resin such as Affi-Gel 501 can be used (Bio-Rad, Hercules, CA).

Alternatively, spleens can be harvested and used in the production of hybridomas to produce monoclonal antibodies following routine methods known in the art as described hereinabove.

#### Example 16: Western Blotting of Tissue Samples

Protein extracts are prepared by homogenizing tissue samples in 0.1 M Tris-HCl (pH 7.5), 15% (w/v) glycerol, 0.2 mM EDTA, 1.0 mM 1,4-dithiothreitol, 10 µg/ml leupeptin and 1.0 mM phenylmethylsulfonylfluoride [Kain et al., Biotechniques, 17:982 (1994)]. Following homogenization, the homogenates are centrifuged at 4°C for 5 minutes to separate supernatant from debris. Debris is reextracted by homogenization with a buffer that is similar to above also contains 0.1 M Tricine and 0.1% SDS. The supernatant from the second extraction is used for Western blotting. For protein quantitation, 2-5 µl of supernatant are added to 1.5 ml of Coomassie Protein Reagent (Pierce, Rockford, IL), and the resulting absorbance at 595 nm is measured.

For SDS-PAGE, samples are adjusted to desired protein concentration with Tricine Buffer (Novex, San Diego, CA), mixed with an equal volume of 2X Tricine sample buffer (Novex, San Diego, CA), and heated for 5 minutes at



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100°C in a thermal cycler. Samples are then applied to a Novex 10-20% Precast Tricine Gel for electrophoresis. Following electrophoresis, samples are transferred from the gels to nitrocellulose membranes in Novex Tris-Glycine Transfer buffer. Membranes are then probed with specific anti-peptide antibodies using the reagents and procedures provided in the Western Lights or Western Lights Plus (Tropix, Bedford, MA) chemiluminescence detection kits. Chemiluminescent bands are visualized by exposing the developed membranes to Hyperfilm ECL (Amersham, Arlington Heights, IL).

Competition experiments are carried out in an analogous manner as above, with the following exception; the primary antibodies (anti-peptide polyclonal antisera) are pre-incubated for 30 minutes at room temperature with varying concentrations of peptide immunogen prior to exposure to the nitrocellulose filter. Development of the Western is performed as above.

After visualization of the bands on film, the bands can also be visualized directly on the membranes by the addition and development of a chromogenic substrate such as 5-bromo-4-chloro-3-indolyl phosphate (BCIP). This chromogenic solution contains 0.016% BCIP in a solution containing 100 mM NaCl, 5 mM MgCl<sub>2</sub> and 100 mM Tris-HCl (pH 9.5). The filter is incubated in the solution at room temperature until the bands develop to the desired intensity. Molecular mass determination is made based upon the mobility of pre-stained molecular weight standards (Novex, San Diego, CA) or biotinylated molecular weight standards (Tropix, Bedford, MA).

#### Example 17: EIA Microtiter Plate Assay

The immunoreactivity of antiserum preferably obtained from rabbits as described in Example 14 was determined by means of a microtiter plate EIA, as follows. Briefly, the BS200 synthetic peptides of SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, and SEQUENCE ID NO 35, prepared as described in Example 10, were dissolved in carbonate buffer (50 mM, pH 9.6) to a final concentration of 2 µg/ml. Next, 100 µl of the peptide or protein solution were placed in each well of an Immulon 2<sup>®</sup> microtiter plate (Dynex Technologies, Chantilly, VA). The plate was incubated overnight at room temperature and then washed four times with deionized water. The wells were blocked by adding 125 µl of a suitable protein blocking agent, such as Superblock<sup>®</sup> (Pierce Chemical Company, Rockford, IL), to each well and then immediately discarding the solution. This blocking procedure was performed

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three times. Antiserum obtained from immunized rabbits or mice, prepared as previously described, was diluted in a protein blocking agent (e.g., a 3% Superblock<sup>®</sup> solution) in PBS containing 0.05% Tween-20<sup>®</sup> (monolaurate polyoxyethylene ether) (Sigma Chemical Company, St. Louis, MO) and 0.05% sodium azide at dilutions of 1:100, 1:500, 1:2500, 1:12,500, and 1:62,500 and placed in each well of the coated microtiter plate. The wells then were incubated for three hours at room temperature. Each well was washed four times with deionized water. One hundred microliters of alkaline phosphatase-conjugated goat anti-rabbit IgG or goat anti-mouse IgG antiserum (Southern Biotech, Birmingham, AB) diluted 1:2000 in 3% Superblock<sup>®</sup> solution in phosphate buffered saline containing 0.05% Tween 20<sup>®</sup> and 0.05% sodium azide, were added to each well. The wells were incubated for two hours at room temperature. Next, each well was washed four times with deionized water. One hundred microliters of paranitrophenyl phosphate substrate (Kirkegaard and Perry Laboratories, Gaithersburg, MD) then were added to each well. The wells were incubated for thirty minutes at room temperature. The absorbance at 405 nm was read in each well. Positive reactions were identified by an increase in absorbance at 405 nm in the test well above that absorbance given by a non-immune serum (negative control). A positive reaction was indicative of the presence of detectable anti-BS200 antibodies. Titers of the anti-peptide antisera were calculated from the previously described dilutions of antisera and defined as the calculated dilution, where  $A_{405\text{nm}}=0.5$  OD.

#### Example 18: Coating of Solid Phase Particles

A. Coating of Microparticles with Antibodies Which Specifically Bind to BS200 Antigen. Affinity purified antibodies which specifically bind to BS200 protein (see Example 15) are coated onto microparticles of polystyrene, carboxylated polystyrene, polymethylacrylate or similar particles having a radius in the range of about 0.1 to 20  $\mu\text{m}$ . Microparticles may be either passively or actively coated. One coating method comprises coating EDAC (1-(3-dimethylaminopropyl)-3-ethylcarbodiimide hydrochloride (Aldrich Chemical Co., Milwaukee, WI) activated carboxylated latex microparticles with antibodies which specifically bind to BS200 protein, as follows. Briefly, a final 0.375% solid suspension of resin washed carboxylated latex microparticles (available from Bangs Laboratories, Carmel, IN or Serodyn, Indianapolis, IN) are mixed in a solution containing 50 mM MES buffer, pH 4.0 and 150 mg/l of affinity

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purified anti-BS200 antibody (see Example 14) for 15 min in an appropriate container. EDAC coupling agent is added to a final concentration of 5.5 µg/ml to the mixture and mixed for 2.5 hr at room temperature.

The microparticles then are washed with 8 volumes of a Tween 20<sup>®</sup>/sodium phosphate wash buffer (pH 7.2) by tangential flow filtration using a 0.2 µm Microgon Filtration module. Washed microparticles are stored in an appropriate buffer which usually contains a dilute surfactant and irrelevant protein as a blocking agent, until needed.

B. Coating of 1/4 Inch Beads. Antibodies which specifically bind to BS200-antigen also may be coated on the surface of 1/4 inch polystyrene beads by routine methods known in the art (Snitman et al., US Patent 5,273,882) and used in competitive binding or EIA sandwich assays.

Polystyrene beads first are cleaned by ultrasonically cleaning them for about 15 seconds in 10 mM NaHCO<sub>3</sub> buffer at pH 8.0. The beads then are washed in deionized water until all fines are removed. Beads then are immersed in an antibody solution in 10 mM carbonate buffer, pH 8 to 9.5. The antibody solution can be as dilute as 1 µg/ml in the case of high affinity monoclonal antibodies or as concentrated as about 500 µg/ml for polyclonal antibodies which have not been affinity purified. Beads are coated for at least 12 hours at room temperature, and then they are washed with deionized water. Beads may be air dried or stored wet (in PBS, pH 7.4). They also may be overcoated with protein stabilizers (such as sucrose) or protein blocking agents used as non-specific binding blockers (such as irrelevant proteins, Carnation skim milk, Superblock<sup>®</sup>, or the like).

#### Example 19: Microparticle Enzyme Immunoassay (MEIA)

BS200 antigens are detected in patient test samples by performing a standard antigen competition EIA or antibody sandwich EIA and utilizing a solid phase such as microparticles (MEIA). The assay can be performed on an automated analyzer such as the IMx<sup>®</sup> Analyzer (Abbott Laboratories, Abbott Park, IL).

A. Antibody Sandwich EIA. Briefly, samples suspected of containing BS200 antigen are incubated in the presence of anti-BS200 antibody-coated microparticles (prepared as described in Example 17) in order to form antigen/antibody complexes. The microparticles then are washed and an indicator reagent comprising an antibody conjugated to a signal generating

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compound (i.e., enzymes such as alkaline phosphatase or horseradish peroxidase) is added to the antigen/antibody complexes or the microparticles and incubated. The microparticles are washed and the bound antibody/antigen/antibody complexes are detected by adding a substrate (e.g., 4-methyl umbelliferyl phosphate (MUP), or OPD/peroxidase, respectively), that reacts with the signal generating compound to generate a measurable signal. An elevated signal in the test sample, compared to the signal generated by a negative control, detects the presence of BS200 antigen. The presence of BS200 antigen in the test sample is indicative of a diagnosis of a breast disease or condition, such as breast cancer.

**B. Competitive Binding Assay.** The competitive binding assay uses a peptide or protein that generates a measurable signal when the labeled peptide is contacted with an anti-peptide antibody coated microparticle. This assay can be performed on the IMx<sup>®</sup> Analyzer (available from Abbott Laboratories, Abbott Park, IL). The labeled peptide is added to the BS200 antibody-coated microparticles (prepared as described in Example 17) in the presence of a test sample suspected of containing BS200 antigen, and incubated for a time and under conditions sufficient to form labeled BS200 peptide (or labeled protein) / bound antibody complexes and/or patient BS200 antigen / bound antibody complexes. The BS200 antigen in the test sample competes with the labeled BS200 peptide (or BS200 protein) for binding sites on the microparticle. BS200 antigen in the test sample results in a lowered binding of labeled peptide and antibody coated microparticles in the assay since antigen in the test sample and the BS200 peptide or BS200 protein compete for antibody binding sites. A lowered signal (compared to a control) indicates the presence of BS200 antigen in the test sample. The presence of BS200 antigen suggests the diagnosis of a breast disease or condition, such as breast cancer.

The BS200 polynucleotides and the proteins encoded thereby which are provided and discussed hereinabove are useful as markers of breast tissue disease, especially breast cancer. Tests based upon the appearance of this marker in a test sample such as blood, plasma or serum can provide low cost, non-invasive, diagnostic information to aid the physician to make a diagnosis of cancer, to help select a therapy protocol, or to monitor the success of a chosen therapy. This marker may appear in readily accessible body fluids such as blood, urine or stool as antigens derived from the diseased tissue which are detectable by immunological methods. This marker may be elevated in a disease state,

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altered in a disease state, or be a normal protein of the breast which appears in an inappropriate body compartment.

Example 20: Immunohistochemical Detection of BS200 Protein

Antiserum against a BS200 synthetic peptide derived from the consensus peptide sequence (SEQUENCE ID NO 31) described in Example 14, above, is used to immunohistochemically stain a variety of normal and diseased tissues using standard procedures. Briefly, frozen blocks of tissue are cut into 6 micron sections, and placed on microscope slides. After fixation in cold acetone, the sections are dried at room temperature, then washed with phosphate buffered saline and blocked. The slides are incubated with the antiserum against a synthetic peptide derived from the consensus BS200 peptide sequence (SEQUENCE ID NO 31) at a dilution of 1:500, washed, incubated with biotinylated goat anti-rabbit antibody, washed again, and incubated with avidin labeled with horseradish peroxidase. After a final wash, the slides are incubated with 3-amino-9-ethylcarbazole substrate which gives a red stain. The slides are counterstained with hematoxylin, mounted, and examined under a microscope by a pathologist.

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We Claim:

1. A method of detecting the presence of a target BS200 polynucleotide in a test sample, comprising:
  - 5 (a) contacting said test sample with at least one BS200-specific polynucleotide or complement thereof; and
  - (b) detecting the presence of said target BS200 polynucleotide in the test sample, wherein said BS200-specific polynucleotide has at least 50% identity with a polynucleotide selected from the group consisting of SEQUENCE ID NOS  
10 1-16, and fragments or complements thereof.
2. The method of claim 1, wherein said target BS200 polynucleotide is attached to a solid phase prior to performing step (a).
- 15 3. A method for detecting mRNA of BS200 in a test sample, comprising:
  - (a) performing reverse transcription with at least one primer in order to produce cDNA;
  - (b) amplifying the cDNA obtained from step (a) using BS200  
20 oligonucleotides as sense and antisense primers to obtain BS200 amplicon; and
  - (c) detecting the presence of said BS200 amplicon, wherein the BS200 oligonucleotides utilized in steps (a) and (b) have at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof.
- 25 4. The method of claim 3, wherein said test sample is reacted with a solid phase prior to performing one of steps (a), (b), or (c).
5. The method of claim 3, wherein said detection step comprises  
30 utilizing a detectable label capable of generating a measurable signal.
6. A method of detecting a target BS200 polynucleotide in a test sample suspected of containing said target, comprising:
  - (a) contacting said test sample with at least one BS200 oligonucleotide  
35 as a sense primer and with at least one BS200 oligonucleotide as an anti-sense primer and amplifying to obtain a first stage reaction product;

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(b) contacting said first stage reaction product with at least one other BS200 oligonucleotide to obtain a second stage reaction product, with the proviso that the other BS200 oligonucleotide is located 3' to the BS200 oligonucleotides utilized in step (a) and is complementary to said first stage reaction product; and

5 (c) detecting said second stage reaction product as an indication of the presence of the target BS200 polynucleotide, wherein the BS200 oligonucleotides utilized in steps (a) and (b) have at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof.

10

7. The method of claim 6, wherein said test sample is reacted with a solid phase prior to performing one of steps (a), (b), or (c).

8. The method of claim 6, wherein said detection step comprises  
15 utilizing a detectable label capable of generating a measurable signal.

9. The method of claim 8, wherein said detectable label is reacted to a solid phase.

20 10. A test kit useful for detecting BS200 polynucleotide in a test sample, comprising a container containing at least one BS200 polynucleotide having at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof.

25 11. A purified polynucleotide or fragment thereof derived from a BS200 gene, wherein said polynucleotide is capable of selectively hybridizing to the nucleic acid of said BS200 gene and has at least 50% identity with a polynucleotide selected from the group consisting of: (a) SEQUENCE ID NOS 1-7, SEQUENCE ID NO 9, SEQUENCE ID NOS 11-12, SEQUENCE ID NOS  
30 14-16, and complements thereof; and (b) fragments of SEQUENCE ID NOS 1-14.

12. The purified polynucleotide of claim 11, wherein said polynucleotide is produced by recombinant techniques.

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13. The purified polynucleotide of claim 11, wherein said polynucleotide is produced by synthetic techniques.

14. The purified polynucleotide of claim 11, wherein said  
5 polynucleotide comprises a sequence encoding at least one BS200 epitope.

15. A recombinant expression system comprising a nucleic acid sequence that includes an open reading frame derived from BS200 operably linked to a control sequence compatible with a desired host, wherein said nucleic acid  
10 sequence has at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof.

16. A cell transfected with the recombinant expression system of claim  
15.

17. A BS200 polypeptide having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.  
20

18. The polypeptide of claim 17, wherein said polypeptide is produced by recombinant techniques.

19. The polypeptide of claim 17, wherein said polypeptide is produced  
25 by synthetic techniques.

20. An antibody which specifically binds to at least one BS200 epitope, wherein said BS200 epitope is derived from an amino acid sequence having at least 50% identity with an amino acid sequence selected from the group  
30 consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

21. An assay kit for determining the presence of BS200 antigen or anti-BS200 antibody in a test sample, comprising a container containing a BS200  
35 polypeptide having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32,



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SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

22. The assay kit of claim 21, wherein said polypeptide is attached to a  
5 solid phase.

23. An assay kit for determining the presence of BS200 antigen in a test sample, comprising a container containing an antibody which specifically binds to a BS200 antigen which comprises at least one BS200 epitope.  
10

24. The kit of claim 23, wherein said antibody is attached to a solid phase.

25. A method for producing a polypeptide comprising at least one  
15 BS200 epitope, said method comprising incubating host cells that have been transfected with an expression vector containing a polynucleotide sequence encoding a polypeptide, wherein said polypeptide comprises an amino acid sequence having at least 50% identity with an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32,  
20 SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

26. A method for detecting BS200 antigen in a test sample suspected of containing said BS200 antigen, comprising:

25 (a) contacting the test sample with an antibody or fragment thereof which specifically binds to at least one epitope of a BS200 antigen selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof, wherein said contacting is carried out for a time and under  
30 conditions sufficient for the formation of antibody/antigen complexes; and  
(b) detecting the presence of said complexes as an indication of the presence of said BS200 antigen.

27. The method of claim 26, wherein said antibody is attached to a  
35 solid phase.

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28. A method for detecting the presence of antibodies specific for a BS200 antigen in a test sample suspected of containing such antibodies, said method comprising:

- (a) contacting the test sample with a BS200 polypeptide, wherein said  
5 BS200 polypeptide contains at least one BS200 epitope derived from an amino acid sequence or fragment thereof having at least 50% identity to an amino acid sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof, and further wherein said  
10 contacting is carried out for a time and under conditions sufficient to allow antigen/antibody complexes to form; and
- (b) detecting the presence of said complexes as an indication of the presence of said antibodies specific for a BS200 antigen.

- 15 29. The method of claim 28, wherein said BS200 polypeptide is attached to a solid phase.

30. A cell transfected with a nucleic acid sequence encoding at least one BS200 epitope, wherein said nucleic acid sequence is selected from the group  
20 consisting of SEQUENCE ID NOS 1-16, and fragments or complements thereof.

31. A method for producing antibodies which specifically bind to BS200 antigen, comprising administering to an individual an isolated immunogenic polypeptide or fragment thereof in an amount sufficient to elicit an  
25 immune response, wherein said immunogenic polypeptide comprises at least one BS200 epitope and has at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

30

32. A method for producing antibodies which specifically bind to BS200 antigen, comprising administering to an individual a plasmid comprising a sequence which encodes at least one BS200 epitope derived from a polypeptide having an amino acid sequence selected from the group consisting of SEQUENCE  
35 ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

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33. A composition of matter comprising a BS200 polynucleotide or fragment thereof, wherein said polynucleotide has at least 50% identity with a polynucleotide selected from the group consisting of: (a) SEQUENCE ID NOS 1-  
5 7, SEQUENCE ID NO 9, SEQUENCE ID NOS 11-12, SEQUENCE ID NOS 14-16, and complements thereof; and (b) fragments of SEQUENCE ID NOS 1-14.

34. A composition of matter comprising a polypeptide containing at  
10 least one BS200 epitope, wherein said polypeptide has at least 50% identity with a sequence selected from the group consisting of SEQUENCE ID NO 31, SEQUENCE ID NO 32, SEQUENCE ID NO 33, SEQUENCE ID NO 34, SEQUENCE ID NO 35, and fragments thereof.

35. The test kit of claim 10 further comprising a container with tools  
15 useful for collection of said sample, wherein the tools are selected from the group consisting of lancets, absorbent paper, cloth, swabs and cups.

36. The assay kit of claim 21 further comprising a container with tools  
20 useful for collection of said sample, wherein the tools are selected from the group consisting of lancets, absorbent paper, cloth, swabs and cups.

37. The test kit of claim 23 further comprising a container with tools  
25 useful for collection of said sample, wherein the tools are selected from the group consisting of lancets, absorbent paper, cloth, swabs and cups.

38. A gene, or a fragment thereof, which codes for a BS200 protein  
having an amino acid sequence with at least 50% identity with SEQUENCE ID  
NO 31.

39. A gene, or a fragment thereof, comprising DNA having at least  
30 50% identity with SEQUENCE ID NO 15 or SEQUENCE ID NO 16.

40. The method of claim 1 wherein presence of said target BS200  
35 polynucleotide in said test sample is indicative of breast disease.

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41. The method of claim 3 wherein presence of said amplicon is indicative of breast disease.

42. The method of claim 6 wherein presence of said second stage  
5 reaction product is indicative of breast disease.

43. The method of claim 26 wherein detection of said complexes is indicative of breast disease.

10 44. The method of claim 28 wherein detection of said complexes is indicative of breast disease.

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>2767006	GTCACCACCA	TCAGGACAAG	TGTAACCTTT	AAGCTAAATG	AAGGCAAGTG
Consensus	GTCACCACCA	TCAGGACAAG	TGTAACCTTT	AAGCTAAATG	AAGGCAAGTG
>2767006	TAGTTTGAAA	AATGCTGAGC	TGTTTCCCGA	GGGTCTGCGA	CCAGCACTAC
Consensus	TAGTTTGAAA	AATGCTGAGC	TGTTTCCCGA	GGGTCTGCGA	CCAGCACTAC
>2767006	CAGAGAAGCA	CAGCTCAGTA	AAAGAGAGCT	TCCGCTACGT	AAACCTTACA
Consensus	CAGAGAAGCA	CAGCTCAGTA	AAAGAGAGCT	TCCGCTACGT	AAACCTTACA
>2767006	TGCAGCTCTG	GCAAGCAAGT	CCCAGGAGCC	CCTGGCCGAC	CAAGCACCCC
Consensus	TGCAGCTCTG	GCAAGCAAGT	CCCAGGAGCC	CCTGGCCGAC	CAAGCACCCC
>2767006	TAAGGAAATG	TTTATCACTG	TTGAGTTTGA	GCTTGAAACT	AACCAAAAGG
>3021177	GGAAATG	TTTATCACTG	TTGAGTTTGA	GCTTGAAACT	AACCAAAAGG
>3021177IH	GGAAATG	TTTATCACTG	TTGAGTTTGA	GCTTGAAACT	AACCAAAAGG
Consensus	TAAGGAAATG	TTTATCACTG	TTGAGTTTGA	GCTTGAAACT	AACCAAAAGG
>2767006	AGGTGACAGC	TTCTTGTGAC			
>3021177	AGGTGACAGC	TTCTTGTGAC	CTGAGCTGCA	TCGTAAAGCG	AACCGAGAAG
>3021177IH	AGGTGACAGC	TTCTTGTGAC	CTGAGCTGCA	TCGTAAAGCG	AACCGAGAAG
>3213801					AG
Consensus	AGGTGACAGC	TTCTTGTGAC	CTGAGCTGCA	TCGTAAAGCG	AACCGAGAAG
>3021177	CGGCTCCGTA	AAGCCATCCG	CATGCTCAGA	AAGGCCGTCC	ACAGGGAGCA
>3021177IH	CGGCTCCGTA	AAGCCATCCG	CATGCTCAGA	AAGGCCGTCC	ACAGGGAGCA
>3213801	CGGCTCCGTA	AAGCCATCCG	CACGCTCAGA	AAGGCCGTCC	ACAGGGAGCA
Consensus	CGGCTCCGTA	AAGCCATCCG	CATGCTCAGA	AAGGCCGTCC	ACAGGGAGCA
>3021177	GTTTCACCTC	CAGCTCTCAG	GCATGAACCT	CGACGTGGCT	AAAAAGCCTC
>3021177IH	GTTTCACCTC	CAGCTCTCAG	GCATGAACCT	CGACGTGGCT	AAAAAGCCTC
>3213801	GTTTCACCTC	CAGCTCTCAG	GCATGAACCT	CGACGTGGCT	AAAAAGCCTC
Consensus	GTTTCACCTC	CAGCTCTCAG	GCATGAACCT	CGACGTGGCT	AAAAAGCCTC
>3021177	CCAGAACATC	TGAACGCCAG	GCAGAGTCCT	GTGGAGTGGG	CCAGGGTCAT
>3021177IH	CCAGAACATC	TGAACGCCAG	GCAGAGTCCT	GTGGAGTGGG	CCAGGGTCAT
>3213801	CCAGAACATC	TGAACGCCAG	GCAGAGTCCT	GTGGAGTGGG	CCAGGGTCAT
Consensus	CCAGAACATC	TGAACGCCAG	GCAGAGTCCT	GTGGAGTGGG	CCAGGGTCAT
>3021177	GCAGAAAACC	AATGTGTCAG	TTGCAGGG		
>3021177IH	GCAGAAAACC	AATGTGTCAG	TTGCAGGGCT	GGGACCTATT	ATGATGGAGC
>3213801	GCAGAAAACC	AATGTGTCAG	TTGCAGGGCT	GGGACCTATT	ATGATGGAGC
Consensus	GCAGAAAACC	AATGTGTCAG	TTGCAGGGCT	GGGACCTATT	ATGATGGAGC
>3021177IH	ACGAGAACGC	TGCATTTTAT	GTCCAAATGG	AACCTTCCAA	AATGAGGAAG
>3213801	ACGAGAACGC	TGCATTTTAT	GTCCAAATGG	AACCTTCCAA	AATGAGGAAG
>224165					GGAAG
Consensus	ACGAGAACGC	TGCATTTTAT	GTCCAAATGG	AACCTTCCAA	AATGAGGAAG
>3021177IH	GACAAATGAC	TTGTGAACCA	TGCCCAAGAC	CAGGAAATTC	TGGGGCCCTG
>3213801	GA				
>224165	GACAAATGAC	TTGTGAACCA	TGCCCAAGAC	CAGGAAATTC	TGGGGCCCTG
Consensus	GACAAATGAC	TTGTGAACCA	TGCCCAAGAC	CAGGAAATTC	TGGGGCCCTG

**FIG. 1A**  
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>3021177IH AAGACCCCAG AAGCTTGGAA TATGTCTGAA TGTGGAGGTC TGTGTCAACC
>2224165   AAGACCCCAG AAGCTTGGAA TATGTCTGAA TGTGGAGGTC TGTGTCAACC
Consensus  AAGACCCCAG AAGCTTGGAA TATGTCTGAA TGTGGAGGTC TGTGTCAACC

>3021177IH TGGTGAATAT TCTGCAGATG GCTTTGCACC TTGCCAGCTC TGTGCCCTGG
>2224165   TGGTGAATAT TCTGCAGATG GCTTTGCACC TTGCCAGCTC TGTGCCCTGG
Consensus  TGGTGAATAT TCTGCAGATG GCTTTGCACC TTGCCAGCTC TGTGCCCTGG

>3021177IH GCACGTTCCA GCCTGAAGCT GGTGCAACTT CCTGCTTCCC CTGTGGAGGA
>2224165   GCACGTTCCA GCCTGAAGCT GGTGCAACTT CCTGCTTCCC CTGTGGAGGA
>1316156   GCACGTTCCA GCCTGAAGCT GGTGCAACTT CCTGCTTCCC CTGTGGAGGA
Consensus  GCACGTTCCA GCCTGAAGCT GGTGCAACTT CCTGCTTCCC CTGTGGAGGA

>3021177IH GGCCTTGCCA CCAAACATCA GGGAGCTACT TCCTTTCAGG ACTGTGAAAC
>2224165   GGCCTTGCCA CCAAACATCA GGGAGCTACT TCCTTTCAGG ACTGTGAAAC
>1316156   GGCCTTGCCA CCAAACATCA GGGAGCTACT TCCTTTCAGG ACTGTGAAAC
Consensus  GGCCTTGCCA CCAAACATCA GGGAGCTACT TCCTTTCAGG ACTGTGAAAC

>3021177IH CAGAGTTCAA TGTTACCTG GACATTTCTA CAACACCACC ACTCACCAT
>1316156   CAGAGTTCAA TGTTACCTG GACATTTCTA NAACACCACC ACTCACCAT
>1549512   CAGAGTTCAA TGTTACCTG GACATTTCTA CAACACCACC ACTCACCAT
Consensus  CAGAGTTCAA TGTTACCTG GACATTTCTA CAACACCACC ACTCACCAT

>3021177IH GTATTCGTTG CCCAGTGGGA ACATACCAGC CTGAATTTGG AAAAAATAAT
>1316156   GTATTCGTTG CCCAGTGGGA ACATACCAGC CTGAATTTGG AAAAAATAAT
>1549512   GTATTCGTTG CCCAGTGGGA ACATACCAGC CTGAATTTGG AAAAAATAAT
Consensus  GTATTCGTTG CCCAGTGGGA ACATACCAGC CTGAATTTGG AAAAAATAAT

>3021177IH TGTGTTTCTT GCCCAGGAAA TACTACGACT GACTTTGATG GCTCCACAAA
>1316156   TGTGTTTCTT GCCCAGGAAA TACTACGACT GACTTTGATG GCTCCACAAA
>1549512   TGTGTTTCTT GCCCAGGAAA TACTACGACT GACTTTGATG GCTCCACAAA
Consensus  TGTGTTTCTT GCCCAGGAAA TACTACGACT GACTTTGATG GCTCCACAAA

>3021177IH CATAACCCAG TGTAAAAACA GAAGATGTGG AGGGGAGCTG GGAGATTTC
>1316156   CATAACCCAG TGTAAAAACA GAAGATGTGG AGGGGAGCTG GGAGATTTC
>1549512   CATAACCCAG TGTAAAAACA GAAGATGTGG AGGGGAGCTG GGAGATTTC
Consensus  CATAACCCAG TGTAAAAACA GAAGATGTGG AGGGGAGCTG GGAGATTTC

>3021177IH CTGGGTACAT TGAATCCCCA AACTACCCAG GCAATTACCC AGCCAACACC
>1549512   CTGGGTACAT TGAATCC
>1919065   CTGGGTACAT TGAATCCCCA AACTACCCAG GCAATTACCC AGCCAACACC
Consensus  CTGGGTACAT TGAATCCCCA AACTACCCAG GCAATTACCC AGCCAACACC

>3021177IH GAGTGTACGT GGACCATCAA CCCACCCCC AAGCGCCGCA TCCTGATCGT
>1919065   GAGTGTACGT GGACCATCAA CCCACCCCC AAGCGCCGCA TCCTGATCGT
Consensus  GAGTGTACGT GGACCATCAA CCCACCCCC AAGCGCCGCA TCCTGATCGT

>3021177IH GGTCCCTGAG ATCTTCCTGC CCATAGAGGA CGACTGTGGG GACTATCTGG
>1919065   GGTCCCTGAG ATCTTCCTGC CCATAGAGGA CGACTGTGGG GACTATCTGG
Consensus  GGTCCCTGAG ATCTTCCTGC CCATAGAGGA CGACTGTGGG GACTATCTGG

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FIG. 1B

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>3021177IH TGATGCGGAA AACCTCTTCA TCCAATTCTG TGACAACATA TGAAACCTGC
>1919065    TGATGCGGAA AACCTCTTCA TNCAATTCTG TGACAACATA T
>g898160    CAACATA TGAAACCTGC
Consensus   TGATGCGGAA AACCTCTTCA TCCAATTCTG TGACAACATA TGAAACCTGC

>3021177IH CAGACCTACG AACGCCCCAT CGCCTTCACC TCCAGGTCAA AGAAGCTGTG
>g898160    CAGACCTACG AACGCCCCAT CGCCTTCACC TCCAGGTCAA AGAAGCTGTG
Consensus   CAGACCTACG AACGCCCCAT CGCCTTCACC TCCAGGTCAA AGAAGCTGTG

>3021177IH GATTCAGTTC AAGTCCAATG AAGGGAACAG CGCTAGAGGG TTCCACGTCC
>g898160    GATTCAGTTC AAGNCCAATG AAGGGAACAG CGCTAGAGGG TTCCACGTCC
Consensus   GATTCAGTTC AAGTCCAATG AAGGGAACAG CGCTAGAGGG TTCCACGTCC

>3021177IH CATACGTGAC ATATGATGAG GACTACCAGG AACTCATTGA AGACACAGTT
>g898160    CATACGTNAC ATATGATGAG GACTACCAGG AACTCATTGA AGACACAGTT
Consensus   CATACGTGAC ATATGATGAG GACTACCAGG AACTCATTGA AGACACAGTT

>3021177IH CGAGATGGCA GGCTCTATGC ATCTGAGAAC CATCAGGAAA TACTTAAGGA
>g898160    CGAGATNGCA GGCTCTATGC ATCTGAGAAC CATCAGGAAA TACTTAAGGA
Consensus   CGAGATGGCA GGCTCTATGC ATCTGAGAAC CATCAGGAAA TACTTAAGGA

>3021177IH TAAGAAACTT ATCAAGGCTC TGTTTGATGT CCTGGCCCAT CCCCAGAACT
>g898160    TAAGAAACTT ATCAAGGCTC TGTTTGATGT CCTGGCCCAT CCCCAGAACT
>2116945    GAAACTT   ATCAAGGCTC TGTTTGATGT CCTGGCCCAT CCCCAGAACT
Consensus   TAAGAAACTT ATCAAGGCTC TGTTTGATGT CCTGGCCCAT CCCCAGAACT

>3021177IH ATTTCAAGTA CACAGCCCAG GAGTCCCGAG AGATGTTTCC AAGATCGTTC
>g898160    ATTTCAAGTA CAC
>2116945    ATTTCAAGTA CACAGCCCAG GAGTCCCGAG ANATGTTTCC AAGATCGTTC
Consensus   ATTTCAAGTA CACAGCCCAG GAGTCCCGAG AGATGTTTCC AAGATCGTTC

>3021177IH ATCCGATTGC TACGTTCCAA AGTGTCCAGG TTTTGTGAGAC CTTACAAATG
>2116945    ATCCGATTGC TACGTTCCAA AGTGTCCAGG TTTTGTGAGAC CTTACAAATG
Consensus   ATCCGATTGC TACGTTCCAA AGTGTCCAGG TTTTGTGAGAC CTTACAAATG

>3021177IH ACTCAGCCCA CGTGCCACTC AATACAAATG TTCTGCTATA GGGTTGGTGG
>2116945    ACTCAGCCCA CGTGCCACTC AATACAAATG TTCTGCTATA GGGTTGGTGG
>g1985883   CTCAGCCCA CGTGCCACTC AATACAAATG TTCTGCTATA GGGTTGGTGG
Consensus   ACTCAGCCCA CGTGCCACTC AATACAAATG TTCTGCTATA GGGTTGGTGG

>3021177IH GACAGAGCTG TCTTCCTTCT GCATGTCAGC ACAGTCGGGT ATTGCTGCCT
>2116945    GACAGAGCTG TCTTCCTTCT GCATGTCAGC ACAGTCGGGT ATTGCTGCCT
>g1985883   GACAGAGCTG TCTTCCTTCT GCATGTNAGC ACAGTCGGGT ATTGCTGCCT
Consensus   GACAGAGCTG TCTTCCTTCT GCATGTCAGC ACAGTCGGGT ATTGCTGCCT

>3021177IH CCCGTATCAG TGA CTCATTA GAGTTCAATT TTTATAGATA ATACAGATAT
>2116945    CCCGTATCAG NGAC
>g1985883   CCCGTATCAG TGA CTCATTA GAGTTCAATT TTNATAGATA ATACAGATAT
Consensus   CCCGTATCAG TGA CTCATTA GAGTTCAATT TTTATAGATA ATACAGATAT

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FIG.1C

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>3021177IH TTTGGTAAAT TGAAC TTGGT TTTTCTTTCC CAGCATCGTG GATGTAGACT
>g1985883 TTTGGTAAAT TGAAC TTGGT TTTTCTTTCC CAGCATCGTG GATGTAGACT
Consensus TTTGGTAAAT TGAAC TTGGT TTTTCTTTCC CAGCATCGTG GATGTAGACT

>3021177IH GAGAATGGCT TTGAGTGGCA TCAGCTTCTC ACTGCTGTGG GCGGATGTCT
>g1985883 GAGAATGGCT TTNAGTGGCA TCAGCTTCTC ACTGCTGTGG GCGGATGTNT
>1925574 GAGAATGGCT TTGAGTGGCA TCAGCTTCTC ACTGCTGTGG GCGGATGTCT
Consensus GAGAATGGCT TTGAGTGGCA TCAGCTTCTC ACTGCTGTGG GCGGATGTCT

>3021177IH TGGATAGATC AAGGGCTGGC TGAGCTGGAC TTTGGTCAGC CTAGGTGAGA
>g1985883 TGGATAGATC AAGGGCTGGC TGAGCTGGAC TTT
>1925574 TGGATAGATC AAGGGCTGGC TGAGCTGGAC TTTGGTCAGC CTAGGTGAGA
Consensus TGGATAGATC AAGGGCTGGC TGAGCTGGAC TTTGGTCAGC CTAGGTGAGA

>3021177IH CTCACCTGTC CTTCTGGGGT CTTACTCCTC CTCAAGGAGT CTGTAGTGGA
>1925574 CTCACCTGTC CTTCTGGGGT CTTACTCCTC CTCAAGGAGT CTGTAGTGGA
>3724828 CTCACCTGTC CTTCTGGGGT CTTACTCCTC CTCAAGGAGT CAGTAGTGGA
Consensus CTCACCTGTC CTTCTGGGGT CTTACTCCTC CTCAAGGAGT CTGTAGTGGA

>3021177IH AAGGAGGCCA CAGAATAAGC TGCTTATTCT GAAACTTCAG CTTCTCTAG
>1925574 AAGGAGGCCA CAGAATAAGC TGCTTATTCT GAAACTTCAG CTTCTCTAG
>3724828 AAGGAGGCCA CAGAATAAGC TGCTTATTCT GAAACTTCAG CTTCTCTAG
<g1444044 C TGCTTATTCT GAAACTTCAG CTTCTCTAG
Consensus AAGGAGGCCA CAGAATAAGC TGCTTATTCT GAAACTTCAG CTTCTCTAG

>3021177IH CCCGGCCCTC TCTAAGGGAG CCCTCTGCAC TCGTGTGCAG GCTCTCACCA
>1925574 CCCGGCCCTC
>3724828 CCCGGCCCTC TCTAAGGGAG CCCTCTGCAC TCGTGTGCAG GCTCTCACCA
<g1444044 CCCGGCCCTC TCTAAGGGAG CCCTCTGCAC TCGTGTGCAG GCTCTCACCA
Consensus CCCGGCCCTC TCTAAGGGAG CCCTCTGCAC TCGTGTGCAG GCTCTCACCA

>3021177IH GGCAGAACAG TCAAGAGGGG AGGGAAGGAG ACCCCTGCAG GCTCCCTCCA
>3724828 GGCAGAACAG GCAAGAGGGG ANGGAAGGAG ACCCCTGCAG GCTCCCTCCA
<g1444044 GGCAGAACAG GCAAGAGGGG AGGGAAGGAG ACCCCTGCAG GCTCCCTCCA
Consensus GGCAGAACAG GCAAGAGGGG AGGGAAGGAG ACCCCTGCAG GCTCCCTCCA

>3021177IH CCCACCTTGA GACCTGGGAG GACTCAGTTT CTCCACAGCC TTCTCCAGCC
>3724828 CCCACCTTGA GACCTGGGAG GACTCAGTTT CTCCACAGCC TTCTCCAGCC
<g1444044 CCCACCTTGA GACCTGGGAG GACTCAGTTT CTCCACAGCC TTCTCCAGCC
Consensus CCCACCTTGA GACCTGGGAG GACTCAGTTT CTCCACAGCC TTCTCCAGCC

>3021177IH TGTGTGATAC AAGTTTGATC CCAGGAAC TT GAGTTCTAAG CAGTGCTCGT
>3724828 TGTGTGATAC AAGTTTGATC CCAGGAAC TT
<g1444044 TGTGTGATAC AAGTTTGATC CCAGGAAC TT GAGTTCTAAG CAGTGCTCGT
Consensus TGTGTGATAC AAGTTTGATC CCAGGAAC TT GAGTTCTAAG CAGTGCTCGT

>3021177IH GA
<g1444044 GAAAAAAAA AGCAGAAAGA ATTAGAAATA AATAAAAACT AAGCACTTCT
>1808382 ACT AAGCACTTCT
Consensus GAAAAAAAA AGCAGAAAGA ATTAGAAATA AATAAAAACT AAGCACTTCT

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**FIG. 1D**  
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<g1444044 GGAGACAT
>1808382 GGAGACATAA TAATGTACAT TTATTGCCAG CCTTCCTCGT TGCAAGCTTC
Consensus GGAGACATAA TAATGTACAT TTATTGCCAG CCTTCCTCGT TGCAAGCTTC

>1808382 CACCCTGCAG CAAATGCACT ATGCTGACTC TCGCACCTTC AGCTGTGCCC
Consensus CACCCTGCAG CAAATGCACT ATGCTGACTC TCGCACCTTC AGCTGTGCCC

>1808382 TCTGACACTC TGCTGGCCAT TGCCTGAGGG ACTGGGGAGT TCAGGTGAAA
Consensus TCTGACACTC TGCTGGCCAT TGCCTGAGGG ACTGGGGAGT TCAGGTGAAA

>1808382 TGTAATTTCC TCAGTGGATG AGAATCATCA ATTGTC
Consensus TGTAATTTCC TCAGTGGATG AGAATCATCA ATTGTC
```

FIG.1E

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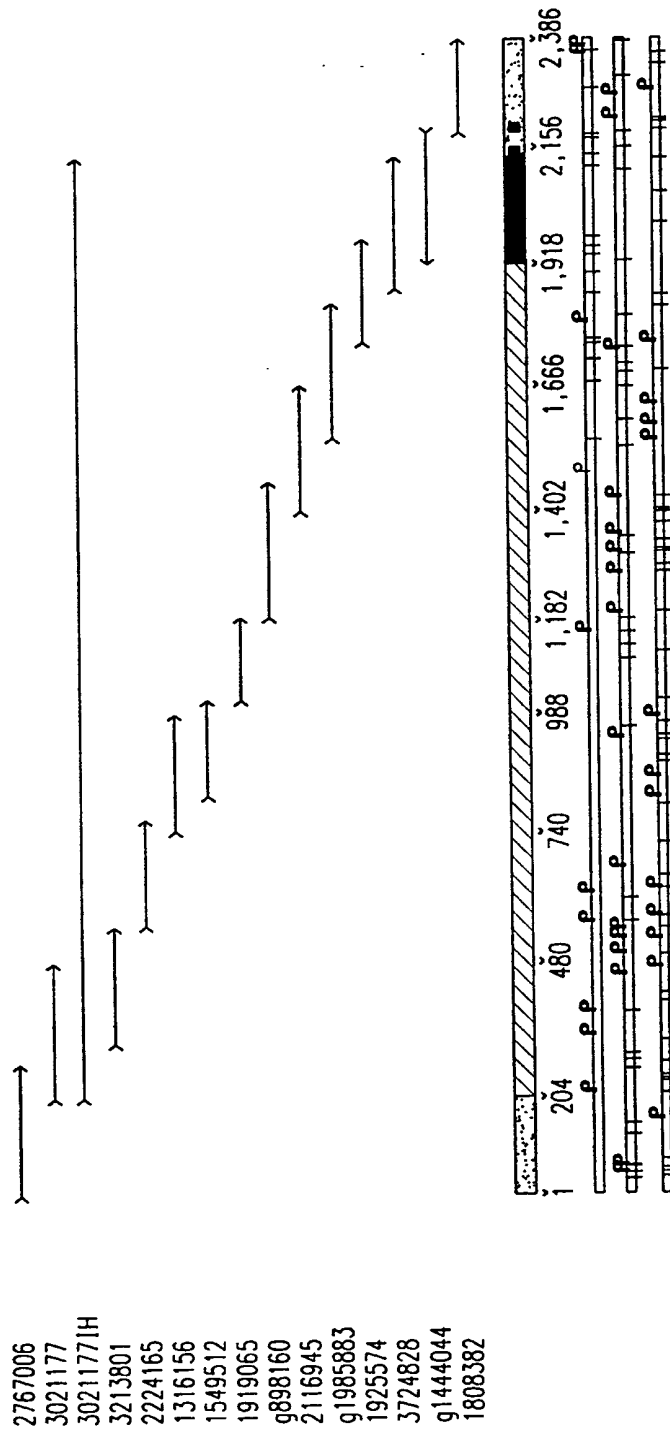


FIG. 2

-1-

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: ABBOTT LABORATORIES
- (ii) TITLE OF THE INVENTION: METHODS AND REAGENTS USEFUL  
FOR DETECTING DISEASES OF THE BREAST
- (iii) NUMBER OF SEQUENCES: 37
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Abbott Laboratories
  - (B) STREET: 100 Abbott Park Road
  - (C) CITY: Abbott Park
  - (D) STATE: IL
  - (E) COUNTRY: USA
  - (F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/889,127
  - (B) FILING DATE: 07-JUL-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Becker, Cheryl L.
  - (B) REGISTRATION NUMBER: 35,441
  - (C) REFERENCE/DOCKET NUMBER: 6130.US.P1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 847/935-1729
  - (B) TELEFAX: 847/938-2623
  - (C) TELEX:

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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCACCACCA TCAGGACAAG TGTAACCTTT AAGCTAAATG AAGGCAAGTG TAGTTTGAAA	60
AATGCTGAGC TGTTTCCCGA GGGTCTGCGA CCAGCACTAC CAGAGAAGCA CAGCTCAGTA	120
AAAGAGAGCT TCCGCTACGT AAACCTTACA TGCAGCTCTG GCAAGCAAGT CCCAGGAGCC	180
CCTGGCCGAC CAAGCACCCC TAAGGAAATG TTTATCACTG TTGAGTTTGA GCTTGAAACT	240
AACCAAAAGG AGGTGACAGC TTCTTGTGAC	270

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGAAATGTTT ATCACTGTTG AGTTTGAGCT TGAAACTAAC CAAAAGGAGG TGACAGCTTC	60
TTGTGACCTG AGCTGCATCG TAAAGCGAAC CGAGAAGCGG CTCCGTAAAG CCATCCGCAT	120
GCTCAGAAAG GCCGTCCACA GGGAGCAGTT TCACCTCCAG CTCTCAGGCA TGAACCTCGA	180
CGTGGCTAAA AAGCCTCCCA GAACATCTGA ACGCCAGGCA GAGTCCTGTG GAGTGGGCCA	240
GGGTCATGCA GAAAACCAAT GTGTCAGTTG CAGGG	275

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCGGCTCCG TAAAGCCATC CGCACGCTCA GAAAGGCCGT CCACAGGGAG CAGTTTCACC	60
TCCAGCTCTC AGGCATGAAC CTCGACGTGG CTAAAAAGCC TCCCAGAACA TCTGAACGCC	120
AGGCAGAGTC CTGTGGAGTG GGCCAGGGTC ATGCAGAAAA CCAATGTGTC AGTTGCAGGG	180
CTGGGACCTA TTATGATGGA GCACGAGAAC GCTGCATTTT ATGTCCAAAT GGAACCTTCC	240
AAAATGAGGA AGGA	254

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAAGGACAA ATGACTTGTG AACCATGCCC AAGACCAGGA AATTCTGGGG CCCTGAAGAC	60
CCCAGAAGCT TGGAAATATGT CTGAATGTGG AGGTCTGTGT CAACCTGGTG AATATTCTGC	120
AGATGGCTTT GCACCTTGCC AGCTCTGTGC CTGGGGCACG TTCCAGCCTG AAGCTGGTGC	180
AACTTCTGTC TTCCCTGTG GAGGAGGCCT TGCCACCAAA CATCA	225

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## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTGGAGGA	GGCCTTGCCA	CCAAACATCA	GGGAGCTACT	TCCTTTCAGG	ACTGTGAAAC	60
CAGAGTTCAA	TGTTACCTG	GACATTTCTA	NAACACCACC	ACTCACCAGT	GTATTCGTTG	120
CCCAGTGGGA	ACATACCAGC	CTGAATTTGG	AAAAAATAAT	TGTGTTTCTT	GCCCAGGAAA	180
TACTACGACT	GACTTTGATG	GCTCCACAAA	CATAACCCAG	TGTAAAAACA	GAAGATGTGG	240
AGGGG						245

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTACCTGG	ACATTTCTAC	AACACCACCA	CTCACCAGTG	TATTCGTTGC	CCAGTGGGAA	60
CATACCAGCC	TGAATTTGGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAAT	ACTACGACTG	120
ACTTTGATGG	CTCCACAAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	180
GAGATTCAC	TGGGTACATT	GAATCC				206

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 162
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAATCCCCA	AACTACCCAG	GCAATTACCC	AGCCAACACC	GAGTGTACGT	GGACNATCAA	60
CCCACCCCC	AAGCGCCGA	TCCTGATCGT	GGTCCCTGAG	ATCTTCCTGC	CCATAGAGGA	120
CGACTGTGGG	GACTATCTGG	TGATGCGGAA	AACCTCTTCA	TNCAATTCTG	TGACAACATA	180
T						181

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## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 81
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 125
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 174
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAACATATGA AACCTGCCAG ACCTACGAAC GCCCCATCGC CTTACCTCC AGGTCAAAGA	60
AGCTGTGGAT TCAGTTCAAG NCCAATGAAG GGAACAGCGC TAGAGGGTTC CAGGTCCCAT	120
ACGTNACATA TGATGAGGAC TACCAGGAAC TCATTGAAGA CATAGTTCGA GATNGCAGGC	180
TCTATGCATC TGAGAACCAT CAGGAAATAC TTAAGGATAA GAACTTATC AAGGCTCTGT	240
TTGATGTCCT GGCCCATCCC CAGAACTATT TCAAGTACAC	280

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 79
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 258
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAACTTATC AAGGCTCTGT TTGATGTCCT GGCCCATCCC CAGAACTATT TCAAGTACAC	60
AGCCCAGGAG TCCCAGAGANA TGTTTCCAAG ATCGTTCATC CGATTGCTAC GTTCCAAAGT	120
GTCCAGGTTT TTGAGACCTT ACAAATGACT CAGCCACGT GCCACTCAAT ACAAATGTTC	180
TGCTATAGGG TTGGTGGGAC AGAGCTGTCT TCCTTCTGCA TGTCAGCACA GTCGGGTATT	240
GCTGCCTCCC GTATCAGNGA C	261

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ix) FEATURE:
  - (A) NAME/KEY: base\_polymorphism
  - (B) LOCATION: 76
  - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
  - (A) NAME/KEY: base\_polymorphism
  - (B) LOCATION: 132
  - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
  - (A) NAME/KEY: base\_polymorphism
  - (B) LOCATION: 212
  - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
  - (A) NAME/KEY: base\_polymorphism
  - (B) LOCATION: 248
  - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCAGCCAC	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	GGTTGGTGGG	ACAGAGCTGT	60
CTTCCTTCTG	CATGTNAGCA	CAGTCGGGTA	TTGCTGCCTC	CCGTATCAGT	GACTCATTAG	120
AGTTCAATTT	TNATAGATAA	TACAGATATT	TTGGTAAATT	GAAGTTGGTT	TTTCTTTCCC	180
AGCATCGTGG	ATGTAGACTG	AGAATGGCTT	TNAGTGGCAT	CAGCTTCTCA	CTGCTGTGGG	240
CGGATGTNTT	GGATAGATCA	AGGGCTGGCT	GAGCTGGACT	TT		282

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGAATGGCT	TTGAGTGGCA	TCAGCTTCTC	ACTGCTGTGG	GCGGATGTCT	TGGATAGATC	60
AAGGGCTGGC	TGAGCTGGAC	TTTGGTCAGC	CTAGGTGAGA	CTCACCTGTC	CTTCTGGGGT	120
CTTACTCCTC	CTCAAGGAGT	CTGTAGTGGA	AAGGAGGCCA	CAGAATAAGC	TGCTTATTCT	180
GAAACTTCAG	CTTCCTCTAG	CCCGGCCCTC				210

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 279 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
  - (A) NAME/KEY: base\_polymorphism
  - (B) LOCATION: 171
  - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCACCTGTCC	TTCTGGGGTC	TTACTCCTCC	TCAAGGAGTC	AGTAGTGGAA	AGGAGGCCAC	60
AGAATAAGCT	GCTTATTCTG	AAACTTCAGC	TTCTCTAGC	CCGGCCCTCT	CTAAGGGAGC	120
CCTCTGCACT	CGTGTGCAGG	CTCTGACCAG	GCAGAACAGG	CAAGAGGGGA	NGGAAGGAGA	180
CCCCTGCAGG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	ACTCAGTTTC	TCCACAGCCT	240
TCTCCAGCCT	GTGTGATACA	AGTTTGATCC	CAGGAACCT			279

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGTCCTCCAG	AAGTGCTTAG	TTTTTATTTA	TTTCTAATTC	TTTCTGCTTT	TTTTTTTCAC	60
GAGCACTGCT	TAGAACTCAA	GTTCTGGGGA	TCAAACCTGT	ATCACACAGG	CTGGAGAAGG	120
CTGTGGAGAA	ACTGAGTCCT	CCCAGGTCTC	AAGGTGGGTG	GAGGGAGCCT	GCAGGGGTCT	180
CCTTCCCTCC	CCTCTTGCTT	GTTCTGCCTG	GTCAGAGCCT	GCACACGAGT	GCAGAGGGCT	240
CCCTTAGAGA	GGGCCGGGCT	AGAGGAAGCT	GAAGTTTCAG	AATAAGCAG		289

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTAAGCACT	TCTGGAGACA	TAATAATGTA	CATTTATTGC	CAGCCTTCCT	CGTTGCAAGC	60
TTCCACCCTG	CAGCAAATGC	ACTATGCTGA	CTCTCGCACC	TTCAGCTGTG	CCCTCTGACA	120
CTCTGCTGGC	CATTGCCTGA	GGGACTGGGG	AGTTCAGGTG	AAATGTAATT	TCCTCAGTGG	180
ATGAGAAATCA	TCAATTGTG					199

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1949 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAATGTTT	ATCACTGTTG	AGTTTGAGCT	TGAAACTAAC	CAAAAGGAGG	TGACAGCTTC	60
TTGTGACCTG	AGCTGCATCG	TAAAGCGAAC	CGAGAAGCGG	CTCCGTAAAG	CCATCCGCAT	120
GCTCAGAAAG	GCCGTCCACA	GGGAGCAGTT	TCACCTCCAG	CTCTCAGGCA	TGAACCTCGA	180
CGTGCGTAAA	AAGCCTCCCA	GAACATCTGA	ACGCCAGGCA	GAGTCCTGTG	GAGTGGGCCA	240
GGGTCATGCA	GAAAACCAAT	GTGTCAGTTG	CAGGGCTGGG	ACCTATTATG	ATGGAGCACG	300
AGAACGCTGC	ATTTTATGTC	CAAATGGAAC	CTTCCAAAAT	GAGGAAGGAC	AAATGACTTG	360
TGAACCATGC	CCAAGACCAG	GAAATTCTGG	GGCCCTGAAG	ACCCAGAAAG	CTTGGAATAT	420
GTCTGAATGT	GGAGGTCTGT	GTC AACCTGG	TGAATATTCT	GCAGATGGCT	TTGCACCTTG	480
CCAGCTCTGT	GCCCTGGGCA	CGTTCCAGCC	TGAAGCTGGT	CGAACTTCCT	GCTTCCCCTG	540
TGGAGGAGGC	CTTGCCACCA	AACATCAGGG	AGCTACTTCC	TTTCAGGACT	GTGAAACCAG	600
AGTTCAATGT	TCACCTGGAC	ATTCTACAA	CACCACCACT	CACCGATGTA	TTCGTTGCCC	660
AGTGGGAACA	TACCAGCCTG	AATTTGGAAA	AAATAATTGT	GTTTCTTGCC	CAGGAAATAC	720
TACGACTGAC	TTTGATGGCT	CCACAAACAT	AACCCAGTGT	AAAAACAGAA	GATGTGGAGG	780
GGAGCTGGGA	GATTTCACTG	GGTACATTGA	ATCCCCAAAC	TACCCAGGCA	ATTACCCAGC	840



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CAACACCGAG	TGTACGTGGA	CCATCAACCC	ACCCCCCAAG	CGCCGCATCC	TGATCGTGGT	900
CCCTGAGATC	TTCCTGCCCC	TAGAGGACGA	CTGTGGGGAC	TATCTGGTGA	TGCGGAAAAC	960
CTCTTCATCC	AATTCTGTGA	CAACATATGA	AACCTGCCAG	ACCTACGAAC	GCCCCATCGC	1020
CTTCACCTCC	AGGTCAAAGA	AGCTGTGGAT	TCAGTTCAAG	TCCAATGAAG	GGAACAGCGC	1080
TAGAGGGTTC	CAGGTCCCAT	ACGTGACATA	TGATGAGGAC	TACCAGGAAC	TCATTGAAGA	1140
CATAGTTCGA	GATGGCAGGC	TCTATGCATC	TGAGAACCAT	CAGGAAATAC	TTAAGGATAA	1200
GAAACTTATC	AAGGCTCTGT	TTGATGTCCT	GGCCCATCCC	CAGAACTATT	TCAAGTACAC	1260
AGCCCAGGAG	TCCCGAGAGA	TGTTTCCAAG	ATCGTTCATC	CGATTGCTAC	GTTCCAAAGT	1320
GTCCAGGTTT	TTGAGACCTT	ACAAATGACT	CAGCCCACGT	GCCACTCAAT	ACAAATGTTT	1380
TGCTATAGGG	TTGGTGGGAC	AGAGCTGTCT	TCCTTCTGCA	TGTCAGCACA	GTCGGGTATT	1440
GCTGCCTCCC	GTATCAGTGA	CTCATTAGAG	TTCAATTTTT	ATAGATAATA	CAGATATTTT	1500
GGTAAATTGA	ACTTGGTTTT	TCTTTCCCAT	CATCGTGGAT	GTAGACTGAG	AATGGCTTTG	1560
AGTGCCTACA	GCTTCTCACT	GCTGTGGGCG	GATGTCTTGG	ATAGATCAAG	GGCTGGCTGA	1620
GCTGGACTTT	GGTCAGCCTA	GGTGAGACTC	ACCTGTCTTT	CTGGGGTCTT	ACTCCTCCTC	1680
AAGGAGTCTG	TAGTGGAAAG	GAGGCCACAG	AATAAGCTGC	TTATTCTGAA	ACTTCAGCTT	1740
CCTCTAGCCC	GGCCCTCTCT	AAGGGAGCCC	TCTGCACTCG	TGTGCAGGCT	CTGACCAGGC	1800
AGAACAGTCA	AGAGGGGAGG	GAAGGAGACC	CTGCGAGGCT	CCCTCCACCC	ACCTTGAGAC	1860
CTGGGAGGAC	TCAGTTTCTC	CACAGCCTTC	TCCAGCCTGT	GTGATACAAG	TTTGATCCCA	1920
GGAACCTGAG	TTCTAAGCAG	TGCTCGTGA				1949

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCACCACCA	TCAGGACAAG	TGTAACCTTT	AAGCTAAATG	AAGGCAAGTG	TAGTTTGAAA	60
AATGCTGAGC	TGTTTCCCGA	GGGTCTGCGA	CCAGCACTAC	CAGAGAAGCA	CAGCTCAGTA	120
AAAGAGAGCT	TCCGCTACGT	AAACCTTACA	TGCAGCTCTG	GCAAGCAAGT	CCCAGGAGCC	180
CCTGGCCGAC	CAAGCACCCC	TAAGGAAATG	TTTATCACTG	TTGAGTTTGA	GCTTGAAACT	240
AACCAAAGG	AGGTGACAGC	TTCTTGTGAC	CTGAGCTGCA	TCGTAAAGCG	AACCGAGAAG	300
CGGCTCCGTA	AAGCCATCCG	CATGCTCAGA	AAGGCCGTCC	ACAGGGAGCA	GTTTCACCTC	360
CAGCTCTCAG	GCATGAACCT	CGACGTGGCT	AAAAAGCCTC	CCAGAACATC	TGAACGCCAG	420
GCAGAGTCCT	GTGGAGTGGG	CCAGGGTCAT	GCAGAAAACC	AATGTGTCAG	TTGCAGGGCT	480
GGGACCTATT	ATGATGGAGC	ACGAGAACGC	TGCATTTTAT	GTCCAAATGG	AACCTTCCAA	540
AATGAGGAAG	GACAAATGAC	TTGTGAACCA	TGCCCAAGAC	CAGGAAATTC	TGGGGCCCTG	600
AAGACCCAG	AAGCTTGGAA	TATGTCTGAA	TGTGGAGGTC	TGTGTCAACC	TGGTGAATAT	660
TCTGCAGATG	GCTTTCACCC	TTGCCAGCTC	TGTGCCCTGG	GCACGTTCCT	GCCTGAAGCT	720
GGTCTCAACT	CCTGCTTCCC	CTGTGGAGGA	GGCCTTGCCA	CCAAACATCA	GGGAGCTACT	780
TCCTTTTCAGG	ACTGTGAAAC	CAGAGTTCAA	TGTTCACTG	GACATTCTA	CAACACCACC	840
ACTCACCGAT	GTATTCTGTT	CCCAGTGGGA	ACATACCAGC	CTGAATTTGG	AAAAAATAAT	900
TGTGTTTCTT	GCCAGGAAA	TACTACGACT	GACTTTGATG	GCTCCACAAA	CATAACCCAG	960
TGTA AAAACA	GAAGATGTGG	AGGGGAGCTG	GGAGATTTC	CTGGGTACAT	TGAATCCCCA	1020
AACTACCCAG	GCAATTACCC	AGCCAACACC	GAGTGTAACG	GGACCATCAA	CCCACCCCCC	1080
AAGCGCCGCA	TCCTGATCGT	GGTCCCTGAG	ATCTTCCTGC	CCATAGAGGA	CGACTGTGGG	1140
GACTATCTGG	TGATGCGGAA	AACCTCTTCA	TCCAATTCTG	TGACAACATA	TGAAACCTGC	1200
CAGACCTACG	AACGCCCCAT	CGCCTTCACC	TCCAGGTCAA	AGAAGCTGTG	GATTGAGTTC	1260
AAGTCCAATG	AAGGGAACAG	CGCTAGAGGG	TTCCAGGTCC	CATACGTGAC	ATATGATGAG	1320
GACTACCAGG	AACCTATTGA	AGACATAGTT	CGAGATGGCA	GGCTCTATGC	ATCTGAGAAC	1380
CATCAGGAAA	TACTTAAGGA	TAAGAACTT	ATCAAGGCTC	TGTTTGATGT	CCTGGCCCAT	1440
CCCCAGAACT	ATTCAAGTA	CACAGCCAG	GAGTCCCAG	AGATGTTTCC	AAGATCGTTT	1500
ATCCGATTGC	TACGTTCCAA	AGTGTCCAGG	TTTTTGAGAC	CTTACAAATG	ACTCAGCCCC	1560
CGTGCCACTC	AATACAAATG	TTCTGCTATA	GGGTGCGTGG	GACAGAGCTG	TCTTCCTTCT	1620
GCATGTCAGC	ACAGTCGGGT	ATTGCTGCCT	CCCGTATCAG	TGACTCATT	GAGTTCAATT	1680
TTTATAGATA	ATACAGATAT	TTTGGTAAAT	TTCGACTTGG	TTTCTTTCC	CAGCATCGTG	1740
GATGTAGACT	GAGAATGGCT	TTGAGTGGCA	TCAGCTTCTC	ACTGCTGTGG	GCGGATGTCT	1800
TGGATAGATC	AAGGGCTGGC	TGAGCTGGAC	TTTGGTCAGC	CTAGGTGAGA	CTCACCTGTC	1860
CTTCTGGGGT	CTTACTCCTC	CTCAAGGAGT	CTGTAGTGG	AAGGAGGCCA	CAGAATAAGC	1920
TGCTTATTCT	GAAACTTCAG	CTTCTCTAG	CCCCGCCCTC	TCTAAGGGAG	CCCTCTGCAC	1980
TCGTGTGACG	GCTCTGACCA	GGCAGAACAG	GCAAGAGGGG	AGGGAAGGAG	ACCCCTGCAG	2040
GCTCCCTCCA	CCCACCTTGA	GACCTGGGAG	GACTCAGTTT	CTCCACAGCC	TTCTCCAGCC	2100

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TGTGTGATAC	AAGTTTGATC	CCAGGAACTT	GAGTTCTAAG	CAGTGCTCGT	GAAAAAAAAA	2160
AGCAGAAAGA	ATTAGAAATA	AATAAAACT	AAGCACTTCT	GGAGACATAA	TAATGTACAT	2220
TTATTGCCAG	CCTTCCTCGT	TGCAAGCTTC	CACCCTGCAG	CAAATGCACT	ATGCTGACTC	2280
TCGCACCTTC	AGCTGTGCCC	TCTGACACTC	TGCTGGCCAT	TGCCTGAGGG	ACTGGGGAGT	2340
TCAGGTGAAA	TGTAATTTCC	TCAGTGATG	AGAATCATCA	ATTGTC		2386

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTAATTCC	CGGGTCGACG	AGCTCACTAG	TCGGCGGCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCCG						68

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCGGATAAC	AATTTACAC	AGGA	24
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## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA	CGGCCAGT	18
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## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCCCAGAACA TCTGAACGCC

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCACTCACC GATGTATTCG

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTCCTGCCCA TAGAGGACGA

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGTCAGC ACAGTCGGGT

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATCTATCCAA GACATCCGCC

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:  
GGACTCCTGG GCTGTGTACT 20
- (2) INFORMATION FOR SEQ ID NO:27: .
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:  
GTTCCCACTG GGCAACGAAT 20
- (2) INFORMATION FOR SEQ ID NO:28:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:  
GGAGGCTTTT TAGCCACGTC 20
- (2) INFORMATION FOR SEQ ID NO:29:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:  
TACAACACCA CCACTCACC 19
- (2) INFORMATION FOR SEQ ID NO:30:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:  
TTCCGCATCA CCAGATAG 18
- (2) INFORMATION FOR SEQ ID NO:31:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 516 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Val	Thr	Thr	Ile	Arg	Thr	Ser	Val	Thr	Phe	Lys	Leu	Asn	Glu	Gly	Lys
1				5					10					15	
Cys	Ser	Leu	Lys	Asn	Ala	Glu	Leu	Phe	Pro	Glu	Gly	Leu	Arg	Pro	Ala
			20					25				30			
Leu	Pro	Glu	Lys	His	Ser	Ser	Val	Lys	Glu	Ser	Phe	Arg	Tyr	Val	Asn
		35					40					45			
Leu	Thr	Cys	Ser	Ser	Gly	Lys	Gln	Val	Pro	Gly	Ala	Pro	Gly	Arg	Pro
	50					55				60					
Ser	Thr	Pro	Lys	Glu	Met	Phe	Ile	Thr	Val	Glu	Phe	Glu	Leu	Glu	Thr
65				70						75				80	
Asn	Gln	Lys	Glu	Val	Thr	Ala	Ser	Cys	Asp	Leu	Ser	Cys	Ile	Val	Lys
			85						90				95		
Arg	Thr	Glu	Lys	Arg	Leu	Arg	Lys	Ala	Ile	Arg	Met	Leu	Arg	Lys	Ala
			100					105					110		
Val	His	Arg	Glu	Gln	Phe	His	Leu	Gln	Leu	Ser	Gly	Met	Asn	Leu	Asp
		115					120					125			
Val	Ala	Lys	Lys	Pro	Pro	Arg	Thr	Ser	Glu	Arg	Gln	Ala	Glu	Ser	Cys
	130					135					140				
Gly	Val	Gly	Gln	Gly	His	Ala	Glu	Asn	Gln	Cys	Val	Ser	Cys	Arg	Ala
145					150					155					160
Gly	Thr	Tyr	Tyr	Asp	Gly	Ala	Arg	Glu	Arg	Cys	Ile	Leu	Cys	Pro	Asn
			165					170						175	
Gly	Thr	Phe	Gln	Asn	Glu	Glu	Gly	Gln	Met	Thr	Cys	Glu	Pro	Cys	Pro
		180					185					190			
Arg	Pro	Gly	Asn	Ser	Gly	Ala	Leu	Lys	Thr	Pro	Glu	Ala	Trp	Asn	Met
		195					200					205			
Ser	Glu	Cys	Gly	Gly	Leu	Cys	Gln	Pro	Gly	Glu	Tyr	Ser	Ala	Asp	Gly
	210					215					220				
Phe	Ala	Pro	Cys	Gln	Leu	Cys	Ala	Leu	Gly	Thr	Phe	Gln	Pro	Glu	Ala
225				230						235					240
Gly	Arg	Thr	Ser	Cys	Phe	Pro	Cys	Gly	Gly	Gly	Leu	Ala	Thr	Lys	His
			245					250						255	
Gln	Gly	Ala	Thr	Ser	Phe	Gln	Asp	Cys	Glu	Thr	Arg	Val	Gln	Cys	Ser
		260						265					270		
Pro	Gly	His	Phe	Tyr	Asn	Thr	Thr	Thr	His	Arg	Cys	Ile	Arg	Cys	Pro
		275				280						285			
Val	Gly	Thr	Tyr	Gln	Pro	Glu	Phe	Gly	Lys	Asn	Asn	Cys	Val	Ser	Cys
	290					295					300				
Pro	Gly	Asn	Thr	Thr	Thr	Asp	Phe	Asp	Gly	Ser	Thr	Asn	Ile	Thr	Gln
305					310					315					320
Cys	Lys	Asn	Arg	Arg	Cys	Gly	Gly	Glu	Leu	Gly	Asp	Phe	Thr	Gly	Tyr
			325					330						335	
Ile	Glu	Ser	Pro	Asn	Tyr	Pro	Gly	Asn	Tyr	Pro	Ala	Asn	Thr	Glu	Cys
		340					345						350		
Thr	Trp	Thr	Ile	Asn	Pro	Pro	Pro	Lys	Arg	Arg	Ile	Leu	Ile	Val	Val
		355				360						365			
Pro	Glu	Ile	Phe	Leu	Pro	Ile	Glu	Asp	Asp	Cys	Gly	Asp	Tyr	Leu	Val
	370					375					380				
Met	Arg	Lys	Thr	Ser	Ser	Asn	Ser	Val	Thr	Thr	Tyr	Glu	Thr	Cys	
385				390						395				400	
Gln	Thr	Tyr	Glu	Arg	Pro	Ile	Ala	Phe	Thr	Ser	Arg	Ser	Lys	Lys	Leu
			405					410						415	
Trp	Ile	Gln	Phe	Lys	Ser	Asn	Glu	Gly	Asn	Ser	Ala	Arg	Gly	Phe	Gln
		420						425					430		
Val	Pro	Tyr	Val	Thr	Tyr	Asp	Glu	Asp	Tyr	Gln	Glu	Leu	Ile	Glu	Asp
		435				440						445			
Ile	Val	Arg	Asp	Gly	Arg	Leu	Tyr	Ala	Ser	Glu	Asn	His	Gln	Glu	Ile
	450					455					460				
Leu	Lys	Asp	Lys	Lys	Leu	Ile	Lys	Ala	Leu	Phe	Asp	Val	Leu	Ala	His
465					470					475					480
Pro	Gln	Asn	Tyr	Phe	Lys	Tyr	Thr	Ala	Gln	Glu	Ser	Arg	Glu	Met	Phe
			485					490						495	

SUBSTITUTE SHEET (RULE 26)

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Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe Leu  
                   500                  505                  510  
 Arg Pro Tyr Lys  
                   515

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Thr Phe Gln Asn Glu Gly Gln Met Thr Cys Glu Pro Cys Pro Arg  
   1                  5                  10                  15  
 Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu Ala Trp  
                   20                  25

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Thr Thr Thr His Arg Cys Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro  
   1                  5                  10                  15  
 Glu Phe Gly Lys Asn Asn Cys Val Ser Cys Pro Gly  
                   20                  25

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp Phe Thr  
   1                  5                  10                  15  
 Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Asn Thr  
                   20                  25                  30  
 Glu Cys Thr Trp Thr Ile Asn Pro Pro Lys Arg Arg  
                   35                  40                  45

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Phe	Thr	Ser	Arg	Ser	Lys	Lys	Leu	Trp	Ile	Gln	Phe	Lys	Ser	Asn	Glu
1				5					10					15	
Gly	Asn	Ser	Ala	Arg	Gly	Phe	Gln	Val	Pro	Tyr	Val	Thr	Tyr	Asp	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
1				5			

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Met	His	Thr	Glu	His
1				5					10					15	
His	His	His	His	His											
				20											

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/13908

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/63 C12N5/10 C07K14/47 C07K16/30 C12Q1/68  
G01N33/53 G01N33/574 G01N33/577 A61K38/17

According to International Patent Classification(IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL Gcg_Geneseq_D:T25603, MATSUBARA AND OKUBO: "GENE SIGNATURE" XP002082662 97.1% identity in 172 bp overlap with Seq. ID 9 and 96.3% identity in 163 bp overlap with Seq. ID 10. ---	1-16, 30, 33, 35-37, 39
X	DATABASE EMBL EMEST7: Hs1171739, 18 March 1997 HILLIER ET AL.: "WashU-Merck EST Project 1997" XP002082616 98.2% identity in 190 bp overlap with Seq. ID 2 and 100.0% identity in 250 bp overlap with Seq.ID 3. --- -/--	11-16, 30, 33, 39



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

## \* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&amp;" document member of the same patent family

Date of the actual completion of the international search

29 October 1998

Date of mailing of the international search report

12/11/1998

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## INTERNATIONAL SEARCH REPORT

Int. Patent Application No

PCT/US 98/13908

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL  EMEST1: Hs698151, 23 June 1995  HILLIER ET AL.: "WashU-Merck EST Project"  XP002082617  88.1% identity in 227 bp overlap with Seq.  ID 4, 97.6% identity in 246 bp overlap  with Seq. ID 5 and 97.6% identity in 207  bp overlap with Seq. ID 6.</p> <p>---</p>	11-16, 30,33,39
X	<p>DATABASE EMBL  Emest10: Hs602250, 4 December 1995  HILLIER ET AL.: "WashU-Merck EST Project"  XP002082618  100.0% identity in 152 bp overlap with  Seq. ID 6 and 98.9% identity in 181 bp  overlap with Seq. ID 7.</p> <p>---</p>	11-16, 30,33,39
X	<p>DATABASE EMBL  Emest7: Hs1171856, 18 March 1997  HILLIER ET AL.: "WashU-Merck EST Project"  XP002082619  98.3% identity in 239 bp overlap with Seq.  ID 8 and 98.9% identity in 178 bp overlap  with Seq.ID 9.</p> <p>---</p>	11-16, 30,33,39
X	<p>DATABASE EMBL  Emest10: Hs647369, 27 June 1996  HILLIER ET AL.: "WashU-Merck EST Project"  XP002082620  98.1% identity in 475 bp overlap with  Seq.ID 15 and Seq.ID 16</p> <p>---</p>	11-16, 30,33,39
X	<p>DATABASE EMBL  Emgss2: Hsb0883, 16 July 1996  EVANS ET AL.: "GENOMIC SEQUENCE SAMPLED  MAP OF CHROMOSOME 11"  XP002082621  92.8% identity in 582 bp overlap with  Seq.ID 15 and Seq.ID 16.</p> <p>---</p>	11-16, 30,33,39
A	<p>WO 96 14877 A (UNIV JOHNS HOPKINS MED)  23 May 1996  see the whole document</p> <p>---</p>	1-44
A	<p>US 5 236 844 A (BASSET PAUL ET AL)  17 August 1993  see the whole document</p> <p>---</p>	1-44
A	<p>WO 95 20681 A (INCYTE PHARMA INC)  3 August 1995  see the whole document</p> <p>---</p>	1-44
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International Application No

PCT/US 98/13908

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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A	WO 95 15334 A (CALIFORNIA PACIFIC MED CENTER) 8 June 1995 see the whole document ---	1-44
A	SCHWARTZ M K: "CURRENT STATUS OF TUMOUR MARKERS" SCANDINAVIAN JOURNAL OF CLINICAL AND LABORATORY INVESTIGATION, vol. 55, no. SUPPL. 221, 1 January 1995, pages 5-14, XP000490502 see the whole document -----	1-44

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Information on patent family members

In tional Application No

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